

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: September 23, 2002, 09:37:55 ; Search time 11.82 Seconds
(without alignments)
360.334 Million cell updates/sec

Title: US-10-019-455A-24
Perfect score: 590
Sequence: 1 HGIPMDRLASKKICADDECV.....RVYQETKVEPTTIDIFFCE 110

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	590	100.0	128	1	OTOR_HUMAN
2	547	92.7	128	1	OTOR_MOUSE
3	477.5	80.9	132	1	OTOR_CHICK
4	390	66.1	133	1	OTOR_RANCA
5	253.5	43.0	131	1	MIA_HUMAN
6	252.5	42.8	130	1	MIA_BOVIN
7	250.5	42.5	130	1	MIA_RAT
8	235.5	39.9	130	1	MIA_MOUSE
9	88.5	15.0	847	1	VAV3_MOUSE
10	86.5	14.7	845	1	VAV3_HUMAN
11	86.5	14.7	847	1	VAV3_HUMAN
12	85.5	14.5	843	1	VAV_MOUSE
13	85.5	14.5	845	1	VAV_MOUSE
14	82.5	14.0	868	1	VAV2_MOUSE
15	81.5	13.8	878	1	VAV2_HUMAN
16	78.5	13.3	1589	1	CC25_YEAST
17	72	12.2	520	1	ITSN_HUMAN
18	71.5	12.1	541	1	ASNH_METJA
19	70.5	11.9	905	1	ZO3_MOUSE
20	69	11.7	392	1	RURE_ACICA
21	69	11.7	444	1	PUR2_METJA
22	69	11.7	670	1	YB2_SCHPO
23	68.5	11.6	505	1	SRK1_SPOLA
24	68.5	11.6	506	1	SRK4_SPOLA
25	68	11.5	162	1	BAR2_CHIPA
26	68	11.5	259	1	YA20_METJA
27	68	11.5	534	1	VL2_HPV37
28	67	11.4	383	1	PLG3_ASPNG
29	67	11.4	509	1	SYE_VTBCH
30	67	11.4	518	1	VL2_HPV08
31	67	11.4	524	1	VL2_HPV17
32	66	11.2	326	1	BAR1_CHIPA
33	66	11.2	518	1	VL2_HPV36

34	66	11.2	898	1	ZO3_CANFA	O62683 canis famil
35	65.5	11.1	425	1	BIOA_SERMA	P36568 serratia ma
36	65.5	11.1	5217	1	HTSI_COCCA	Q01886 cochliobolu
37	65	11.0	169	1	PIIB_HAEIN	P44499 haenophilus
38	65	11.0	518	1	VL2_HPV47	P22425 human papil
39	65	11.0	933	1	ZO3_HUMAN	O95049 homo sapien
40	64.5	10.9	342	1	LVC_CLOPE	P26836 clostridium
41	64.5	10.9	520	1	DRTS_LEIAM	P16126 leishmania
42	64.5	10.9	659	1	AMIA_STRPN	P18791 streptococc
43	64	10.8	359	1	YKA7_CAEEL	P34258 caenorhabdl
44	64	10.8	433	1	DHOM_BACSU	P19582 bacillus su
45	64	10.8	803	1	CDAAL_BACTU	Q45755 bacillus th

ALIGNMENTS

RESULT 1	OTOR_HUMAN	STANDARD;	PRT;	128 AA.
ID	OTOR_HUMAN			
AC	Q9NRC9;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Otopaplin precursor (Fibrocyte-derived protein) (Melanoma inhibitory activity like protein).			
GN	OTOR OR FDP OR MIAL.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cochlea;			
RA	MEDLINE=20334619; PubMed=10873378;			
RA	Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,			
RA	Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;			
RT	"A novel conserved cochlear gene, OTOR: identification, expression analysis, and chromosomal mapping."			
RL	Genomics 66:242-248(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	MEDLINE=20568254; PubMed=10998416;			
RA	Cohen-Salmon M., Frenz D., Liu W., Verpy E., Voegelting S., Petit C.;			
RT	"Fdp, a new fibrocyte-derived protein related to MIA/CD-RAP, has an in vitro effect on the early differentiation of the inner ear mesenchyme."			
RL	J. Biol. Chem. 275:40036-40041(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain, and Cochlea;			
RA	MEDLINE=21100875; PubMed=11161796;			
RA	Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;			
RT	"Identification and characterization of an inner ear-expressed human melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent polymorphism that abolishes translation."			
RL	Genomics 71:40-52(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavriles G., Almeida J.P., Babbage A.K., Bagguley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,			
RA	Coulson A., Coville G.J., Deadman R., Dhani P., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,			
RA	Lehvaslahti M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,			

```

[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=20334619; PubMed=10873378;
RA Robertson N.G., Heller S., Lin J.S., Resendes B.L., Weremowicz S.,
RA Denis C.S., Bell A.M., Hudspeth A.J., Morton C.C.;
RT "A novel conserved cochlear gene, OTOR: identification, expression
RT analysis, and chromosomal mapping.";
RL Genomics 66:242-248(2000).
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=21100875; PubMed=11161796;
RA Rendtorff N.D., Frodin M., Attie-Bitach T., Vekemans M., Tommerup N.;
RT "Identification and characterization of an inner ear-expressed human
RT melanoma inhibitory activity (MIA)-like gene (MIAL) with a frequent
RT polymorphism that abolishes translation.";
RL Genomics 71:40-52(2001).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN COCHLEA.
CC -1- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-----
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CC EMBL; AF233333; AAF82079.1; -.
CC EMBL; AJ243939; CAC27444.1; -.
CC GMD; MGI:1888678; Otor.
CC InterPro: IPR001452; SH3.
CC SMART; SM00326; SH3; 1.
CC PROSITE; PS50002; SH3; 1.
KW SIGNAL; SH3 domain.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 128 OTORAPLIN.
FT DOMAIN 39 110 SH3.
FT FT FT FT FT BY SIMILARITY.
FT DISULFID 55 127 BY SIMILARITY.
FT SEQUENCE 128 AA; 14328 MW; 3DD47D4C77C4A7FD CRC64;
SQ
Query Match 92.7%; Score 547; DB 1; Length 128;
Best Local Similarity 90.0%; Pred. No. 2.3e-50;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 1 HGFMDRASKKLCADCECVYTISLASAQEDYNAPDCRFNVKVGQOIYVYSKLVKNGA 60
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
19 HGVFMGLSSKKLCADCECVYTISLARAQEDYNAPDCRFIDVRKKGQIYVYSKLVKNGA 78
QY 61 GEFWAGSVYGDGDMGVGVYFPRNLVKQORVQEATKEVPTTIDIFFCE 110
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
79 GEFWAGSVYGDGDMGVGVYFPRNLVKQORVQEATKEIPTTIDIFFCE 128
RESULT 3
OTOR_CHICK STANDARD; PRT; 132 AA.
AC Q918P6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Otoraplin precursor.
GN OTOR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]

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[illegible]

Db

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Proc. Natl. Acad. Sci. U.S.A. 98:5515-5520(2001).
-!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO
AS WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
INFREQUENTLY IN GLIOMA CELL LINES.
-!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
-!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN
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EMBL; X75450; CAA53203.1; -
EMBL; X84707; CAA59195.1; -
EMBL; BC005910; AAH05910.1; -
PDB; 1IIJ; 16-MAY-01.
MIM; 601340; -
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3 domain; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 131
FT DOMAIN 43 113
FT DISULFID 36 41
FT DISULFID 59 130
FT SEQUENCE 131 AA; 14509 MW; 4D3BB30BD6008BDC CRC64;
SQ
Query Match 43.0%; Score 253.5; DB 1; Length 131;
Best Local Similarity 45.4%; Pred. No. 1.1e-19;
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;
QY 5 MDRLASKKLCADDECVYITSLASQAQEDYNAPDCRFNVKKGQIYVYKLVKENGAGE-F 63
DB 27 MPLADRKLCADQESHPISVAVALQDYVAPDCRFITIHGQVYVYFSKL---KGRGLF 83
QY 64 WAGSVYGDGDEMGV-VGYFPRNLVKEQRYQVQATKEVPTTIDDFCE 110
DB 84 WGSVGVGDYGDLAARLGIFPSSIVREDQTLKPGKVDVTKDWDFYCQ 131
RESULT 6
MIA_BOVIN STANDARD; PRT; 130 AA.
AC Q28038;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDRAPI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H., Sandell L.J.;
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
RL during chondrogenesis.";
J. Biol. Chem. 271:3311-3316(1996).
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CC -!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
MAINTENANCE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -!- INDUCTION: REPPRESSED BY RETINOIC ACID.
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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EMBL; U51437; AAC48523.1; -
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
Growth factor; Signal; SH3 domain.
FT SIGNAL 1 22
FT CHAIN 23 130
FT DOMAIN 42 112
FT DISULFID 35 40
FT DISULFID 58 129
FT SEQUENCE 130 AA; 14353 MW; 95D153161C78E02A CRC64;
SQ
Query Match 42.8%; Score 252.5; DB 1; Length 130;
Best Local Similarity 45.0%; Pred. No. 1.4e-19;
Matches 50; Conservative 22; Mismatches 28; Indels 11; Gaps 4;
QY 5 MDRLASKKLCADDECVYITSLASQAQEDYNAPDCRFNVKKGQIYVYKLVKENGAGE-F 63
DB 26 MPLADRKMCADDECSHPISVAVALQDYVAPDCRFITIHGQVYVYFSKL---KGRGLF 82
QY 64 WAGSVYGDGDEMGV-VGYFPRNLVKEQRYQVQATKEVPTTIDDFCE 110
DB 83 WGSVGVGDYGDGAARL---GYFPSSIVREDQTLKPAKTDVTKDWDFYCQ 130
RESULT 7
MIA_RAT STANDARD; PRT; 130 AA.
AC Q62946; P97591;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDRAPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Mammary gland;
RA Lu J.X.;
RT "Gene expression changes associated with chemically-induced rat
RT mammary carcinogenesis.";
RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 34-124 FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=96216414; PubMed=8621736;
RA Dietz U.H., Sandell L.J.;
RT "Cloning of a retinoic acid-sensitive mRNA expressed in cartilage and
```

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RT during chondrogenesis."
RL J. Biol. Chem. 271:3311-3316(1996).
CC -!- FUNCTION: MAY FUNCTION DURING CARTILAGE DEVELOPMENT AND
CC MAINTENANCE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: CARTILAGE PRIMORDIA AND CARTILAGE.
CC -!- INDUCTION: REPPRESSED BY RETINOIC ACID.
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
EMBL; U51438; AAC52481.1; -
EMBL; U67884; AAB40659.1; -
InterPro; IPR001452; SH3.
Pfam; PF00018; SH3; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; FALSE NEG.
Growth factor; Signal; SH3 domain.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
FT PROTEIN.
FT DOMAIN 42 112 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 129 BY SIMILARITY.
FT CONFLICT 46 47 MA -> VT (IN REF. 2).
FT SEQUENCE 130 AA; 14536 MW; 5F99149AECF74501 CRC64;
FT SQ
Query Match 42.5%; Score 250.5; DB 1; Length 130;
Best Local Similarity 44.4%; Pred. No. 2.2e-19;
Matches 48; Conservative 23; Mismatches 32; Indels 5; Gaps 3;
QY 5 MDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGE-F 63
Db 26 MPKLDWKLCADDECSHPISMAVALQDYVAPDCRFITIRGVQVYVFSKL---KGRGRLF 82
QY 64 WAGSVYGDQDEMGV-VGFPPRNLVKEQRYQEAETKVEPTTIDIDFCE 110
Db 83 WGSVQGGYGYDLAHLGFFPSSIVREDTLTKPGKIDMKTDWDFYQ 130
ULT 8
MIA_MOUSE
ID MIA_MOUSE STANDARD; PRT; 130 AA.
AC Q61865; P97495; O09086;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Melanoma derived growth regulatory protein precursor (Melanoma
DE inhibitory activity) (Cartilage-derived retinoic acid-sensitive
DE protein) (CD-RAP).
GN MIA OR CDRAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RX MEDLINE=95007612; PubMed=7923218;
RA Blesch A., Bossertoff A.-K., Apfel R., Behl C., Hessdoerfer B.,
RA Schmitt A., Jachmickzak P., Lottspeich F., Buettner R., Bogdahn U.;
RT "Cloning of a novel malignant melanoma-derived growth-regulatory
RT protein, MIA."
RL Cancer Res. 54:5695-5701(1994).
```

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RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=97251341; PubMed=9097023;
RX Bossertoff A.K., Kondo S., Moser M., Dietz U., Copeland N.G.,
RA Gilbert D.J., Jenkins N.A., Buettner R., Sandell L.J.;
RA "Mouse CD-RAP/MIA gene: structure, chromosomal localization, and
RT expression in cartilage and chondrosarcoma.";
RL Dev. Dyn. 208:516-525(1997).
CC -!- FUNCTION: ELICITS GROWTH INHIBITION ON MELANOMA CELLS IN VITRO AS
CC WELL AS SOME OTHER NEUROECTODERMAL TUMORS, INCLUDING GLIOMAS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: ALL MALIGNANT MELANOMA CELL LINES TESTED AND
CC INFREQUENTLY IN GLIOMA CELL LINES.
CC -!- PTM: MAY POSSESS TWO INTRAMOLECULAR DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO THE MIA / OTOR FAMILY.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
EMBL; X94322; CAA63983.1; -
EMBL; U85612; AAB42082.1; -
DR EMBL; X97965; CAA66608.1; -
DR MGD; MGI:109615; Cdrap.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00018; SH3; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; FALSE NEG.
DR Growth factor; Signal; SH3 domain.
KW SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 130 MELANOMA DERIVED GROWTH REGULATORY
FT PROTEIN.
FT DOMAIN 42 112 SH3.
FT DISULFID 35 40 BY SIMILARITY.
FT DISULFID 58 129 BY SIMILARITY.
FT CONFLICT 112 113 TL -> NS (IN REF. 1).
FT SEQUENCE 130 AA; 14593 MW; 16C957459C5BB5F9 CRC64;
FT SQ
Query Match 39.9%; Score 235.5; DB 1; Length 130;
Best Local Similarity 43.5%; Pred. No. 8.1e-18;
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;
QY 5 MDRLASKKLCADDECYVTTISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENGAGE-F 63
Db 26 MPKLDWKLCADDECSHPISMAVALQDYVAPDCRFITIRGVQVYVFSKL---KGRGRLF 82
QY 64 WAGSVYGDQDEMGV-VGFPPRNLVKEQRYQEAETKVEPTTIDIDFCE 110
Db 83 WGSVQGGYGYDLAHLGFFPSSIVREDTLTKPGKIDMKTDWDFYQ 130
RESULT 9
VAV3_MOUSE
ID VAV3_MOUSE STANDARD; PRT; 847 AA.
AC Q9R0C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE VAV-3 protein.
GN VAV3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

SEQUENCE FROM N.A.
Trenkle T., McClelland M., Welsh J.;
Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: EXCHANGE FACTOR FOR GTP-BINDING PROTEINS RHOA, RHOG AND,
TO A LESSER EXTENT, RAC-1. BINDS PHYSICALLY TO THE NUCLEOTIDE-FREE
STATES OF THOSE GTPASES (BY SIMILARITY).
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
-!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
BINDING DOMAIN.
-!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
-!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.

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EMBL; AF067816; AAF09171.1; -
HSSP; PI2931; IAIE.
DR MGD; MGI:1888518; Vav3.
DR InterPro: IPR003247; CH type.
DR InterPro: IPR001715; Calponin_hom.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR001331; GDS_CDC24.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000219; RhoGEF.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR003096; SM22_calponin.
DR Pfam: PF00307; CH; 1.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00621; RhoGEF; 1.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00888; SM22CALPONIN.
DR ProDom: PD001527; CH type; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain; Repeat;
KW Guanine-nucleotide releasing factor.
FT DOMAIN 1 119
FT DOMAIN 192 371
FT DOMAIN 400 502
FT DOMAIN 514 562
FT DOMAIN 552 660
FT DOMAIN 672 766
FT DOMAIN 788 847
SQ SEQUENCE 847 AA; 97946 MW; 9AGB63F0D9E60F8F CRC64;

Query Match

15.0%; Score 88.5; DB 1; Length 847;

Best Local Similarity 31.3%; Pred. No. 0.14;
Matches 21; Conservative 14; Mismatches 21; Indels 11; Gaps 2;
QY 23 ISLASAQEDYNAPDCRFINVKKQQIIVVSKLVKENGAGEFWAGSYGDCQDENGVGVF 82
DB 790 LGIATARYPCARDMRELSLLKGMVKIYTKM-----SANGWWRGEVNGR-----VGWF 838
QY 83 PRNLVKE 89
DB 839 PSTYVEE 845

RESULT 10
ID VAV_HUMAN STANDARD; PRT; 845 AA.
AC P15198; Q15860;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE VAV proto-oncogene.
GN VAV1 OR VAV.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA DenKinger D.J., Borges C.R., Shaw C.L., Cushman A.M., Kawahara R.S.;
RT "Transcriptional regulation of the vav proto-oncogene."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 62-845 FROM N.A.
RX MEDLINE=90005432; PubMed=2477241;
RA Katza S., Martin-Zanca D., Barbacid M.;
RT "vav, a novel human oncogene derived from a locus ubiquitously
expressed in hematopoietic cells."
RL EMBO J. 8:2283-2290(1989).
RN [3]
RP SEQUENCE OF 1-61 FROM N.A.
RX MEDLINE=91172176; PubMed=2005887;
RA Katza S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
oncogene activates its transforming potential."
RL Mol. Cell. Biol. 11:1912-1920(1991).
RN [4]
RP SEQUENCE OF 299-837 FROM N.A.
RA Romero F.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 299-334 FROM N.A.
RX MEDLINE=96038895; PubMed=7478592;
RA Ramos-Morales F., Romero F., Schweighoffer F., Bismuth G., Camonis J.,
RA Tortolero M., Fischer S.;
RT "The proline-rich region of vav binds to Grb2 and Grb3-3."
RL Oncogene 11:1665-1669(1995).
RN [6]
RP SIMILARITY TO CDC24 FAMILY.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.M., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
with the dbl GDP-GTP exchange factor, the bcr gene and a yeast gene
(CDC24) involved in cytoskeletal organization."
RL Oncogene 7:611-618(1992).
CC -!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
BINDING PROTEIN. CAN BE ACTIVATED BY TRUNCATION OF THE N-TERMINUS.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
NOT IN OTHER CELL TYPES.
CC -!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
BINDING DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.


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DR PROSITE: PS50001; SH2: 1.
DR PROSITE: PS50002; SH3: 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
FT Guanine-nucleotide releasing factor; Repeat.
FT DOMAIN 1 119 CH.
FT DOMAIN 194 373 PH.
FT DOMAIN 402 504 PH.
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 615 658 SH3 1.
FT DOMAIN 669 763 SH2.
FT DOMAIN 780 840 SH3 2.
SQ SEQUENCE 843 AA; 97953 MW; C4A5ACAD45FCB80E CRC64;

Query Match 14.5%; Score 85.5; DB 1; Length 843;
Best Local Similarity 31.4%; Pred. No. 0.29;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASQAEDYNAPDCRFNVKKGQOIYVSKLVKENGAGFEWAGSVYGDQDEMVGVPFPRN 85
      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
      785 AKARYDFCARDSELSLKEGDII----KILNKKGGQGWWRGEIYGR-----IGWFPSPN 833

QY 86 LVKEQRVQOE 95
      I I I I I
DB 834 YVEED--YSE 841

RESULT 13
VAV_MOUSE STANDARD; PRT; 845 AA.
AC P27870;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE VAV proto-oncogene.
GN VAV1 OR VAV.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92228488; PubMed=1565462;
RA Adams J.A., Houston H., Allen J., Lints T., Harvey R.;
RT "The hematopoietically expressed vav proto-oncogene shares homology
RT with the dbi GTP-GTP exchange factor, the bcr gene and a yeast gene
RT (CDC24) involved in cytoskeletal organization.";
RT (Oncogene 7:611-618(1992)).
RX MEDLINE=91172176; PubMed=2005887;
RA Katav S., Cleveland J.L., Heslop H.E., Pulido D.;
RT "Loss of the amino-terminal helix-loop-helix domain of the vav proto-
RT oncogene activates its transforming potential.";
RL Mol. Cell. Biol. 11:1912-1920(1991).
CC -!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
CC -!- BINDING PROTEIN. CAN BE ACTIVATED BY TRUNCATION OF THE N-TERMINUS.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN HEMATOPOIETIC CELLS BUT
CC NOT IN OTHER CELL TYPES.
CC -!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DBI-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
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CC -----
DR EMBL; X64361; CAA45713.1; -.
DR EMBL; M59833; AAA63402.1; -.
DR PIR; A39576; A39576.
DR HSP; S36941; S36941.
DR HSP; P29354; IGRI.
DR TRANSFAC; T01230; -.
DR MGD; MGI:98923; Vav.
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR001715; Calponin_hom.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00008; DAGPEDOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRODOM; PD001527; CH_type; 1.
DR SMART; SM00109; Cl; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS50021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS50010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Proto-oncogene; Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat.
FT DOMAIN 1 119 CH.
FT DOMAIN 194 373 DH.
FT DOMAIN 402 504 PH.
FT DOMAIN 516 564 PHORBOL-ESTER AND DAG BINDING.
FT DOMAIN 617 660 SH3 1.
FT DOMAIN 671 765 SH2.
FT DOMAIN 782 842 SH3 2.
FT CONFLICT 29 29 Q -> E (IN REF. 2).
SQ SEQUENCE 845 AA; 98136 MW; 3666DCCDIC5229DA CRC64;

Query Match 14.5%; Score 85.5; DB 1; Length 845;
Best Local Similarity 31.4%; Pred. No. 0.29;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASQAEDYNAPDCRFNVKKGQOIYVSKLVKENGAGFEWAGSVYGDQDEMVGVPFPRN 85
      I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
      787 AKARYDFCARDSELSLKEGDII----KILNKKGGQGWWRGEIYGR-----IGWFPSPN 835

DB 787 AKARYDFCARDSELSLKEGDII----KILNKKGGQGWWRGEIYGR-----IGWFPSPN 835

QY 86 LVKEQRVQOE 95
      I I I I I
DB 836 YVEED--YSE 843

RESULT 14
VAV2_MOUSE STANDARD; PRT; 868 AA.
ID VAV2_MOUSE
AC Q60992;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
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DE VAV-2 protein.
GN VAV2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=1090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=96313271; PubMed=8710375;
RA Schuebel K.E., Bustelo X.R., Nielsen D.A., Song B.J., Barbacid M.,
RA Goldman D., Lee I.J.;
RT "Isolation and characterization of murine vav2, a member of the vav
family of proto-oncogenes.";
RL Oncogene 13:363-371(1996).
CC -!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
CC BINDING PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U37017; AAC52761.1; .
DR HSSP; G60631; 1GBQ.
DR MGD; MGI:102718; Vav2.
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR001715; Calponin_hom.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 2.
DR PRINTS; PR00452; SH3DOMAIN.
DR ProDom; PD001527; CH_type; 1.
DR SMART; SM00109; C1; 1.
DR SMART; SM00033; CH; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00235; RhoGEF; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 2.
DR PROSITE; PS00021; CH; 1.
DR PROSITE; PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE; PS00081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE; PS00010; DH_2; 1.
DR PROSITE; PS00741; DH_1; 1.
DR PROSITE; PS50003; PH_DOMAIN; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 2.
KW Phorbol-ester binding; Zinc; SH2 domain; SH3 domain;
KW Guanine-nucleotide releasing factor; Repeat.
FT DOMAIN 1 119
FT DOMAIN 193 371
FT DOMAIN 400 502
FT DOMAIN 514 562
FT DOMAIN 576 642
SH3 1.

FT DOMAIN 663 757 SH2.
FT DOMAIN 806 867 SH3 2.
SQ SEQUENCE 868 AA; 99915 MW; D18581E7EB2DBC2 CRC64;

Query Match 14.0%; Score 82.5; DB 1; Length 868;
Best Local Similarity 27.6%; Pred. NO. 0.61;
Matches 21; Conservative 20; Mismatches 22; Indels 13; Gaps 3;

QY 20 VVT---ISLASAQEDYNAPDCRFINNVKKQQIYVYVSKLVKENGAGEFWAGSVYGGQDEM 76
Db 802 VTPRVIGTAVARYNFAARDMRELSREGDVVYKYSRIGGDGQ---WMKG-----ETN 851
QY 77 GVVGYPFRNLVKEQVR 92
Db 852 GRIGWFPSTYYEEGV 867

RESULT 15
VAV2_HUMAN
ID VAV2_HUMAN STANDARD; PRT; 878 AA.
AC P52735;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE VAV-2 protein.
GN VAV2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95283235; PubMed=7762982;
RA Henske E.P., Short M.P., Jozwiak S., Bovey C.M., Ramlakhan S.,
RA Haines J.L., Kwiatkowski D.J.;
RT "Identification of VAV2 on 9q34 and its exclusion as the tuberous
RT sclerosis gene TSC1.";
RL Ann. Hum. Genet. 59:25-37(1995).
CC -!- FUNCTION: PROBABLE EXCHANGE FACTOR FOR A SMALL RAS-LIKE GTP-
CC BINDING PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 CALPONIN-HOMOLOGY (CH) DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOMAIN (DH).
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG
CC BINDING DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
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CC -----
DR EMBL; S76992; AAB34377.1; .
DR HSSP; P08631; 1BUL.
DR MIM; 600428; .
DR InterPro; IPR003247; CH_type.
DR InterPro; IPR001715; Calponin_hom.
DR InterPro; IPR002219; DAG_PE-bind.
DR InterPro; IPR001331; GDS_CDC24.
DR InterPro; IPR001849; PH.
DR InterPro; IPR000219; RhoGEF.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR Pfam; PF00307; CH; 1.
DR Pfam; PF00130; DAG_PE-bind; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 14:51:06 ; Search time 49.48 Seconds
(without alignments)
1638.219 Million cell updates/sec

Title: US-10-019-455A-23
Perfect score: 330
Sequence: 1 catggaattatttgacgg.....atattgactctcttcgcgag 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

al number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	DB	ID	Description			
1	63.4	19.2	459	1	US-08-578-649-1	Sequence 1, Appli			
2	63.2	19.2	581	1	US-08-578-649-4	Sequence 4, Appli			
3	57.4	17.4	330	1	US-08-578-649-18	Sequence 18, Appl			
4	54.2	16.4	305	1	US-08-578-649-8	Sequence 8, Appli			
5	40.4	12.2	596	1	US-08-578-649-24	Sequence 24, Appl			
6	40.4	12.2	3565	1	US-08-578-649-3	Sequence 3, Appli			
7	34	10.3	7218	1	US-08-232-463-14	Sequence 14, Appl			
8	33.6	10.2	1136	4	US-08-860-820-1	Sequence 1, Appli			
9	33.6	10.2	1929	4	US-09-359-161-4	Sequence 4, Appli			
10	33.6	10.2	2159	3	US-08-286-870A-7	Sequence 7, Appli			
11	31.2	9.5	4403765	4	US-09-103-840A-2	Sequence 2, Appl			
12	31.2	9.5	4411529	4	US-09-103-840A-1	Sequence 1, Appl			
13	30.8	9.3	1736	4	US-09-360-197-13	Sequence 13, Appl			
14	30.4	9.2	289	4	US-09-007-005-17	Sequence 17, Appl			
15	30.4	9.2	289	4	US-09-244-796-17	Sequence 17, Appl			
16	29.6	9.0	1000	4	US-09-018-584A-38	Sequence 38, Appl			
17	29.4	8.9	2718	4	US-09-651-656-14	Sequence 14, Appl			
18	29.2	8.8	3101	2	US-08-868-786-1	Sequence 1, Appli			
19	28.6	8.7	1518	2	US-08-929-501-4	Sequence 4, Appli			
20	28.6	8.7	1518	2	US-08-929-501-5	Sequence 5, Appli			
21	28.6	8.7	1518	3	US-09-140-177-4	Sequence 4, Appli			
22	28.6	8.7	1518	3	US-09-140-177-5	Sequence 5, Appli			
23	28.6	8.7	1518	4	US-09-397-979-4	Sequence 4, Appli			
24	28.6	8.7	1518	4	US-09-397-979-5	Sequence 5, Appli			
25	28.6	8.7	1753	2	US-08-929-501-1	Sequence 1, Appli			
26	28.6	8.7	1753	2	US-08-929-501-3	Sequence 3, Appli			
27	28.6	8.7	1753	3	US-09-140-177-1	Sequence 1, Appli			

28	28.6	8.7	1753	3	US-09-140-177-3	Sequence 3, Appli
29	28.6	8.7	1753	4	US-09-397-979-1	Sequence 1, Appli
30	28.6	8.7	1753	4	US-09-397-979-3	Sequence 3, Appli
31	28.6	8.7	1770	2	US-08-929-501-11	Sequence 11, Appl
32	28.6	8.7	1770	2	US-08-929-501-13	Sequence 13, Appl
33	28.6	8.7	1770	3	US-09-140-177-11	Sequence 11, Appl
34	28.6	8.7	1770	3	US-09-140-177-13	Sequence 13, Appl
35	28.6	8.7	1770	4	US-09-397-979-11	Sequence 11, Appl
36	28.6	8.7	1770	4	US-09-397-979-13	Sequence 13, Appl
37	28.6	8.7	2073	2	US-08-929-501-25	Sequence 25, Appl
38	28.6	8.7	2073	2	US-08-929-501-26	Sequence 26, Appl
39	28.6	8.7	2073	3	US-09-140-177-25	Sequence 25, Appl
40	28.6	8.7	2073	3	US-09-140-177-26	Sequence 26, Appl
41	28.6	8.7	2073	4	US-09-397-979-25	Sequence 25, Appl
42	28.6	8.7	2073	4	US-09-397-979-26	Sequence 26, Appl
43	28.6	8.7	2153	4	US-09-367-206-6	Sequence 6, Appli
44	28.6	8.7	2576	3	US-09-265-108-1	Sequence 1, Appli
45	28.6	8.7	2576	4	US-09-479-264-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-578-649-1
; Sequence 1, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 40..432
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 40..111
; FEATURE:

REGISTRATION NUMBER: 31,575


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Query Match      12.2%; Score 40.4; DB 1; Length 596;
Best Local Similarity 63.3%; Pred. No. 0.00087;
Matches 62; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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RESULT      6
US-08-578-649-3
; Sequence 3, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 4805 Third Avenue
; CITY: New York

```

	Query Match	12.2%	Score 40.4;	DB 1;	Length 3585;
	Best Local Similarity	63.3%;	Pred. No. 0.002;		
	Matches 62;	Conservative	0;	Mismatches 36;	Indels 0;
	Gaps	0;			
Qy	65	ctatttcctggctagtcctcaagaagattataatgcccggactgtagattcattaaacg	124		
Dh	1589	CTATCTCCATGGCTGTGCGCTTCAGACTACATGCGCCCGACTGGCATCTCTGACCA	1648		

```

      1589  C T A T T C C A T G G T G T G G C C C T T C A G A C T A C A T G G C C C C C C G A
      162  T T A A A A A A G G C A G C A G A T C A T G T G A C T C A A A G C T G
      1649  T T C A C C G G G C C A A G T G T G T G T C T C T T C C A A G C T G
      1686

RESULT 7
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHREIFLINGER, F.

```



```
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
; FEATURE:
; OTHER INFORMATION: Lycopersicon esculentum plant homolog of yeast
; OTHER INFORMATION: SNE1 kinase subunit of protein kinase (LeSNF1)
US-09-359-161-4

Query Match
Best Local Similarity 10.2%; Score 33.6; DB 4; Length 1929;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 84 tcaagagagattataatgccccggagctgtagattcattacgttaaaagggcagagat 143
Db 1793 TCTGTAAGTAGACTGTAGGTAACTGAAATTCATAAACGTTAAAAAGAGAGAGT 1734
144 ctatgtgtactcaaaagctgttaaaagaaatggagctggagaaattttggcctggcagtgt 203
Db 1733 AGATCTCCTAGCGAATCAAAAGAAAAAGAGTTGCTAGGCACCTCTGACCAAGAGGGT 1674

QY 204 ttatggtgatggccag 219
Db 1673 GGAATTTGTTAAACAAG 1658
```

```
RESULT 10
US-08-286-870A-7/c
; Sequence 7, Application US/08286870A
; Patent No. 6063605
; GENERAL INFORMATION:
; APPLICANT: ELY, S
; APPLICANT: TAILOR, RH
; APPLICANT: TIPPETT, JM
; APPLICANT: BLENK, RG
; TITLE OF INVENTION: BACTERIAL GENES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN DARBY & CUSHMAN
; ADDRESSEE: Intellectual Property Group of
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,870A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/520228
; FILING DATE: 09-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8910624.9
; FILING DATE: 09-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL N. KOKULIS
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: 70608/220720
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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```
; LENGTH: 2159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2159
US-08-286-870A-7

Query Match
Best Local Similarity 10.2%; Score 33.6; DB 3; Length 2159;
Matches 75; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 174 tggagctggagaattttggcgtggcagtggtttatgtgtatggccagagacagatgggagt 233
Db 2002 TGGTGTGTGAACAGAGGGCGGTGACCTTCTCCTGGGCCTTCTCGAAGTCGTACTCGGCT 1943

QY 234 cgtgggtttttcccccaggaacttggtcaagggaacagcgtgtgtaccaggaagctaccaa 293
Db 1942 CGTAGTCACTCCACGGGCACGAACTCGATGCGGTGATGATACACTCGTTGCCGCTGC 1883

QY 294 ggaagttccaccacggatattga 317
Db 1882 TGAAGTTCAGGCGCGCGATGGTGA 1859
```

```
RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
```

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Query Match
Best Local Similarity 9.5%; Score 31.2; DB 4; Length 4403765;
Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 99 tgcgccggagctgttagattcattaaacgtttaaaagggcagcagatctatgttactcaaa 158
Db 426225 tgtccagcggggccgagcgtcccccgcattgcagggtgatcgaccgacggggccaaga 426284

QY 159 gctgttaaaagaaatggagcgtggagaattttggcgtgcagtggttatgttgatggcca 218
Db 426285 cgggtccactgaggatgcctatgtcgacgcttcgcgtggcgtatctctgggaaacgttaa 426344

QY 219 ggacgagatgggagtcgtggttatttccccaggaacttggtcaaggaacagcgtgtgta 278
Db 426345 tggcggggatggagacatgtgtatgcgcgtgtggtgggagcgttgacgggatgtcga 426404

QY 279 ccagggaag 286
```

Db 426405 cattgagg 426412

RESULT 12

US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 9.5%; Score 31.2; DB 4; Length 4411529;
Best Local Similarity 47.9%; Pred. No. 34;
Matches 90; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

Qy 99 tccccgcgactgaattcattaaacgttaaaaaaggcagcagatctgttactcaaa 158
Db 426067 tctccagcgggcccacgcgtcccgccatcgaggtgatcgaccggggccaaga 426126

Qy 159 gctgttaaaagaaatggagctggagaattttgggctggcagtggtttatggatggcca 218
Db 426127 cggtcacctgaggatgctatgtcagcgtccctcgtcgtcgtatctggggaacgtaa 426186

Qy 219 ggacgagatgggctgctgggttatttcccccaggaaacttggtcaaggaaacgctgtgta 278
Db 426187 tggcggggtgagacattggtgctgcgcggtgatggggtatgacccggatgtcga 426246

Qy 279 ccaggaag 286
Db 426247 cattgagg 426254

RESULT 13

US-360-197-13/C
; Sequence 13, Application US/09360197
; Patent No. 6287859
; GENERAL INFORMATION:
; APPLICANT: Bassilana, Frederic
; APPLICANT: Lazdunski, Michel
; APPLICANT: Waldmann, Rainer
; APPLICANT: Deweille, Jan R.
; TITLE OF INVENTION: Human and Rat Families of Neuronal Acid-Sensitive
; TITLE OF INVENTION: Cationic Channels, Their Cloning and Applications
; FILE REFERENCE: 989.6706P
; CURRENT APPLICATION NUMBER: US/09/360.197
; CURRENT FILING DATE: 1997-07-23
; PRIOR APPLICATION NUMBER: 09/129,758
; PRIOR FILING DATE: 1998-08-05
; PRIOR APPLICATION NUMBER: 60/095,408
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1736
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-360-197-13

Query Match 9.3%; Score 30.8; DB 4; Length 1736;
Best Local Similarity 63.5%; Pred. No. 1.8;
Matches 47; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 247 ccaggaacttggtcaaggaacagcgtgtgtaccaggaaagctaccaggaagtctccacc 306
Db 533 CCCACAAGGTTGGCCACCGAAGCAGTCCAGCAGCATGTCTATCCAGGAGTGCCCGC 474

Qy 307 acggatattgactt 320
Db 473 ACGGGCATAGATT 460

RESULT 14

US-09-007-005-17
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350003
; CURRENT APPLICATION NUMBER: US/09/007.005B
; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 289
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17

Query Match 9.2%; Score 30.4; DB 4; Length 289;
Best Local Similarity 6.6%; Pred. No. 1.1;
Matches 16; Conservative 96; Mismatches 130; Indels 0; Gaps 0;

Qy 56 gtgtctactattctctgtgctagtgtctcaagaagattataatgcccgactgtat 115
Db 27 rururarcrarururarcrarurgrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnr 86

Qy 116 tcattaaacttaaaaaaggcagcagatctatgttactcaaaagctggtaaaagaaatg 175
Db 87 rnrrnr 146

Qy 176 gagctggagaatttggcgtggcagtggtttatggtatggtccagcagcagatggagtcg 235
Db 147 rnrrnr 206

Qy 236 tgggttatttccccgaacttggtcaagaaacagcgtgtgtaccaggaagctaccaag 295
Db 207 rnrrnr 266

Qy 296 aa 297
Db 267 aa 268

RESULT 15

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US-09-244-796-17
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; TITLE OF INVENTION: FUSIONS
; FILE REFERENCE: 00786/350007
; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Translation template
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(289)
OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

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Query Match          9.2%; Score 30.4; DB 4; Length 289;
Best Local Similarity 6.6%; Pred. No. 1.1;
Matches 16; Conservative 96; Mismatches 130; Indels 0; Gaps 0;

Qy 56 gtgtctactattctctgtgtagtgcacgaagattataatgcccgactgtagat 115
Db   : : : | : : : | : : : | : : : | : : : | : : : | : : : |
27 ruruurarcrarururarcrarurgrnrnrnrnrnrnrnrnrnrnrnrnrnr 86

Qy 116 tcattaacgttaaaaaaggcgacgacgtatgtgtactcaagctggtaaaaaatg 175
Db   : : : : : : : : : : : : : : : : : : : : : : : : : :
87 rnrrsrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnr 146

Qy 176 gagctggagaatttggcgtggcagttttatgtggcagcagcagatgggagtcg 235
Db   : : : : : : : : : : : : : : : : : : : : : : : : : :
147 rnrrsrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnr 206

236 tgggttattcccgaggactgtgtcaggaacagcgtgtgtaccaggaagctaccaagg 295
Db   : : : | : : | : : | : : | : : | : : | : : | : : |
207 rnrrsrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnrnr 266

Qy 296 aa 297
Db 267 aa 268

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Search completed: September 23, 2002, 15:39:48
Job time: 2922 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 14:24:26 ; Search time 1961.35 Seconds
(without alignments)
3520.920 Million cell updates/sec

Title: US-10-019-455a-23

Perfect score: 330

Sequence: 1 catggaattatttgaccg.....atattgactttcttgcgag 330

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

al number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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ALIGNMENTS

RESULT 1

BD010816

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD010816 330 bp DNA linear PAT 31-JAN-2002
Novel polypeptide and DNA thereof.

BD010816

BD010816.1 GI:18639189

JP 2001069994-A/17.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 330)

Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,

Yoshimura, K. and Tanaka, H.

Novel polypeptide and DNA thereof

Patent: JP 2001069994-A 17 21-MAR-2001;

TAKEEDA CHEMICAL INDUSTRIES LTD

OS Homo sapiens (human)

PN JP 2001069994-A/17

PD 21-MAR-2001

PF 29-JUN-2000 JP 2000195911

PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI

SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
CC
CC C12P21/08, C12N15/00, A61K37/02, C12N5/00

Key Location/Qualifiers
FH source 1..330
FT /organism='Homo sapiens (human)'.
FT Location/Qualifiers

FEATURES
source
1..330
/organism='Homo sapiens'
/db_xref='taxon:9606'
BASE COUNT 91 a 60 c 91 g 88 t
ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 330;
Best Local Similarity 100.0%; Pred. No. 3e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catggaattattatgaccgtctagcttccaagaagctctgtgcagatgatgagtgtgc 60
|||||
Db 1 CATGGAATATTTATGACCCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 60
QY 61 tatactatttctgtgctagctcaagaagattataatgccccggactgtgattcatt 120
|||||
Db 61 TATACTATTCTCTGCTAGTCTCAAGAAGATTATAATGCCCCGACTGTAGATTCATT 120
QY 121 aacgttaaaaggcagcagatctctgtactcaaaagctggttaaaagaatggagct 180
|||||
Db 121 AACGTTAAAAAGGCGCAGAGATCTATGTCTACTAAAGCTGTGTAAGAAAAATGGAGCT 180
QY 181 ggaagaatttggctgacgttttatgtgatgcccagacagatggagctgtggt 240
|||||
Db 181 GGAAATTTGGCTGGCAGTGTATGTGTATGGCCAGACGAGATGGAGTGTGGGT 240
QY 241 tatttccccagaaacttggctcaaggacagcgtgtgtaccagaaagctaccaggaagtt 300
|||||
Db 241 TATTTCCTCCAGGAACCTGTGTCAGGAACACAGCGTGTGTACCAGGAAGCTACCAAGGAAGTT 300
QY 301 cccaccacggatattgaacttcttctgcgag 330
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Db 301 CCCACCACGGATATTGACTTCTCTCCGAG 330

RESULT 2
LOCUS BD010802 384 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010802
VERSION BD010802.1 GI:18639175
KEYWORDS JP 2001069994-A/3.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 3 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Homo sapiens (human)
PN JP 2001069994-A/3
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA

PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
G01N33/53//
PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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FT Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 3.1e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 55 CATGGAATATTTATGACCCTCTAGCTTCCAAGAAGCTCTGTGCAGATGATGAGTGTGC 114
QY 61 tatactatttctgtgctagctcaagaagattataatgccccggactgtgattcatt 120
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QY 121 aacgttaaaaggcagcagatctctgtactcaaaagctggttaaaagaatggagct 180
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Db 175 AACGTTAAAAAGGCGCAGAGATCTATGTCTACTAAAGCTGTGTAAGAAAAATGGAGCT 234
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QY 241 tatttccccagaaacttggctcaaggacagcgtgtgtaccagaaagctaccaggaagtt 300
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QY 301 cccaccacggatattgaacttcttctgcgag 330
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Db 355 CCCACCACGGATATTGACTTCTCTCCGAG 384

RESULT 3
LOCUS AF233261 846 bp mRNA linear PRI 06-JUL-2000
DEFINITION Homo sapiens otoraplin (OTOR) mRNA, complete cds.
ACCESSION AF233261
VERSION AF233261.1 GI:8927427
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 846)
AUTHORS Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,
Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
TITLE A Novel Conserved Cochlear Gene, OTOR: Identification, Expression
Analysis, and Chromosomal Mapping
JOURNAL Genomics 66 (3), 242-248 (2000)
PUBMED 10873378
REFERENCE 2 (bases 1 to 846)
AUTHORS Robertson, N.G., Heller, S., Lin, J.S., Resendes, B.L., Weremowicz, S.,
Denis, C.S., Bell, A.M., Hudspeth, A.J., and Morton, C.C.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-2000) Pathology, Brigham and Women's Hospital, 75
Francis Street, Boston, MA 02115, USA
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BASE COUNT 235 a 147 c 205 g 259 t
ORIGIN

Query Match 100.0%; Score 330; DB 9; Length 846;
Best Local Similarity 100.0%; Pred. No. 3.4e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 ggagaatttggcgtgagctgttatgtatgtgccagacagatggagtcgtgaggt 240
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Db 279 GGAGAAATTTGGCTGGCAGTGTATGTATGGTGGCCAGACGAGATGGAGTGGTGGGT 338
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Db 399 CCCACCACGGATATTGACTTCTTCTCGCAG 428

RESULT 4
LOCUS AF243505 865 bp mRNA linear PRI 26-DEC-2000
DEFINITION Homo sapiens fibrocyte-derived protein (FDP) mRNA, complete cds.
ACCESSION AF243505
VERSION AF243505.1 GI:11991843
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
Cohen-Salmon, M., Frenz, D., Liu, W., Verpy, E., Voegelings, S. and
Petit, C.
Fdp, a New Fibrocyte-derived Protein Related to MIA/CD-RAP, Has an
in Vitro Effect on the Early Differentiation of the Inner Ear
Mesenchyme
J. Biol. Chem. 275 (51), 40036-40041 (2000)
10998416
2 | (bases 1 to 865)
Cohen-Salmon, M., Frenz, D., Verpy, E., Voegelings, S. and Petit, C.
Direct Submission
Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue

du Dr. Roux, Paris 75015, France
Location/Qualifiers
1. 865
/organism="Homo sapiens"
/db_xref="taxon:9606"
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SAQEDNAPDCRFINVKQQIYVYSLVKENGAGFAGFVAGSVYGDQEMGVGVFPR
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BASE COUNT 258 a 145 c 207 g 255 t
ORIGIN

FEATURES
Source
du Dr. Roux, Paris 75015, France
Location/Qualifiers
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BASE COUNT 258 a 145 c 207 g 255 t
ORIGIN

Query Match 100.0%; Score 330; DB 9; Length 865;
Best Local Similarity 100.0%; Pred. No. 3.4e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 301 cccacacggatattgactttcttcgcgag 330
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Db 362 CCCACCACGGATATTGACTTCTTCTCGCAG 391

RESULT 5
LOCUS BD010820 923 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010820
VERSION BD010820.1 GI:18639193
KEYWORDS JP 2001069994-A/21.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
Ito, Y., Nishi, K., Ogi, K., Okubo, S., Mogi, S., Noguchi, Y.,
Yoshimura, K. and Tanaka, H.
Novel polypeptide and DNA thereof
Patent: JP 2001069994-A 21 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
OS Homo sapiens (human)
PN JP 2001069994-A/21
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
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PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
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CH Key Location/Qualifiers
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 330; DB 6; Length 923;
Best Local Similarity 100.0%; Pred. No. 3.5e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS

6

HS242552

DEFINITION Homo sapiens mRNA for melanoma inhibitory activity like protein (MIAL gene).

ACCESSION AJ242552

VERSION 1.1

KEYWORDS melanoma inhibitory activity like protein; Mial gene.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1422)
AUTHORS Rendtorff,N.D., Frolin,M., Attie-Bitach,T., Vekemans,M. and Tommerup,N.

TITLE Identification and Characterization of an Inner Ear-Expressed Human Melanoma Inhibitory Activity (MIA)-like Gene (MIAL) with a Frequent Polymorphism That Abolishes Translation

JOURNAL Genomics 71 (1), 40-52 (2001)
MEDLINE 21100875
REFERENCE 2 (bases 1 to 1422)
AUTHORS Rendtorff,N.D.

TITLE Direct Submission

JOURNAL Submitted (21-MAY-1999) Rendtorff N.D., Department of Medical

REMARK
COMMENT Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
Revised by author 03-AUG-1999
Related sequence: AJ242552 (Mus musculus mRNA)
Related sequences: AJ252324 to AJ252327 (genomic sequence).

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exon

intron

exon

intron

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BASE COUNT

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Db 355 CCAACCACGGATATTGACTTCTTCTGTGA 383

RESULT 9
AF243504
LOCUS AF243504 929 bp mRNA linear ROD 26-DEC-2000
DEFINITION Mus musculus fibrocyte-derived protein (Fdp) mRNA, complete cds.
ACCESSION AF243504
VERSION AF243504.1 GI:11991841
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 929)
AUTHORS Cohen-Salmon,M., Frenz,D., Liu,W., Verpy,E., Voegeling,S. and
Petit,C.
TITLE Fdp, a New Fibrocyte-derived Protein Related to MIA/CD-RAP, Has an
in Vitro Effect on the Early Differentiation of the Inner Ear
Mesenchyme
JOURNAL J. Biol. Chem. 275 (51), 40036-40041 (2000)
PUBMED 10998416
REFERENCE 2 (bases 1 to 929)
AUTHORS Cohen-Salmon,M., Frenz,D., Verpy,E., Voegeling,S. and Petit,C.
TITLE Direct Submission
JOURNAL Submitted (09-MAR-2000) Biotechnologies, Institut Pasteur, 25 rue
du Dr. Roux, Paris 75015, France
FEATURES
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Query Match 76.4%; Score 252.2; DB 10; Length 929;
Best Local Similarity 85.4%; Pred. No. 7.6e-65;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Qy 301 cccacacagggatattgactctcttcgcga 329
Db 363 CCAACCACGGATATTGACTTCTTCTGTGA 391

RESULT 10
BD010821
LOCUS BD010821 947 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010821
VERSION BD010821.1 GI:18639194
KEYWORDS JP 2001069994-A/22.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 947)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 22 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Mus sp. (mouse)
PN JP 2001069994-A/22
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR
PI YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P9/00, A61P19/02, PC
A61P19/08,
PC C07K14/47, C07K16/18, C12N1/21, C12N5/10, G01N33/15, G01N33/50, PC
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PC C12P21/08, C12N15/00, A61K37/02, C12N5/00
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BASE COUNT 279 a 158 c 221 g 289 t
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Best Local Similarity 85.4%; Pred. No. 7.6e-65;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Db 185 GATGTCAGAAAGGCGACGAGATCTATGTTACTTCAAGCTGGTAAACAGAAACGAGCT 244
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RESULT 11
MMU243939 958 bp mRNA linear ROD 29-JAN-2001
LOCUS Mus musculus mRNA for melanoma inhibitory activity-like protein
DEFINITION AJ243939
ACCESSION AJ243939
VERSION 1 GI:12619174
KEYWORDS melanoma inhibitory activity-like protein; Mial gene.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 958)
AUTHORS Rendorff,N.D., Frodin,M., Attie-Bitach,T., Vekemans,M. and Tommerup,N.

TITLE Identification and Characterization of an Inner Ear-Expressed Human Melanoma Inhibitory Activity (MIA)-like Gene (MIAL) with a Frequent Polymorphism That Abolishes Translation
JOURNAL Genomics 71 (1), 40-52 (2001)
MEDLINE 21100875
REFERENCE 2 (bases 1 to 958)
AUTHORS Rendorff,N.D.

TITLE Direct Submission
JOURNAL Submitted (20-JUL-1999) Rendorff N.D., Department of Medical Genetics, Institute of Medical Biochemistry and Genetics, Blegdamsvej 3, 2200 Copenhagen N, DENMARK
COMMENT Related sequence: AJ242552.

FEATURES
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/organism="Mus musculus"
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/tissue_type="whole fetus"
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24..410
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/db_xref="GI:12619175"

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QY 301 ccacacacgagatattgactctcttcgcga 329
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Db 365 CCAACACCGATATTGACTTCTTCTGTGA 393
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RESULT 12
AF233333 1054 bp mRNA linear ROD 06-JUL-2000
LOCUS Mus musculus otoraplin mRNA, complete cds.
DEFINITION AF233333
ACCESSION AF233333
VERSION 1 GI:8927429
KEYWORDS house mouse.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 1054)
AUTHORS Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
TITLE A Novel Conserved Cochlear Gene, OTOR: Identification, Expression Analysis, and Chromosomal Mapping
JOURNAL Genomics 66 (3), 242-248 (2000)
MEDLINE 10873378
REFERENCE 2 (bases 1 to 1054)
AUTHORS Robertson,N.G., Heller,S., Lin,J.S., Resendes,B.L., Weremowicz,S., Denis,C.S., Bell,A.M., Hudspeth,A.J. and Morton,C.C.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2000) Pathology, Brigham and Women's Hospital, 75 Francis Street, Boston, MA 02115, USA

FEATURES
Location/Qualifiers
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/db_xref="GI:8927430"

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Best Local Similarity 85.4%; Pred. No. 7.8e-65;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Db 72 CATGGTATTATTATGGATAAACTTCTTCTAAGAAGTTGTGCGGATGAGGAGTGTC 131
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QY 61 tatactattctctggctagctccaagaagattatatgcccgagcttagattcatt 120
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Db 132 TATACATATTCTCTGCGACAGACAGGAGATTACAATGCCCGGAGCTGTAGGTTTCATC 191
QY 121 aacgttaaaaaagggcagcagatctatgttactcaaaagctgttaaaagaaatggagct 180
Db 192 GATGTCAGAAAGGGCAGAGATCTATGTTTACTCCAGCTGGTAACAGAAACGGAGCT 251
QY 181 ggagaattttggctggcagtggtttatgtgtatggccagagacagatgggagtcgtgggt 240
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Db 312 TATTTCCCGCAACCTTGGTGAAGAGCAGCGGTATACAGGAGGCCCAAGGAGATC 371
QY 301 ccaccacggatattgactctctctgcga 329
Db 372 CCAACCCAGGATATTGACTTCTCTGTGA 400

RESULT 13

BD010836 330 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010836
VERSION BD010836.1 GI:18639209
KEYWORDS JP 2001069994-A/37.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 330)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 37 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/37
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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FT /organism='Rattus sp. (rat)'.
LOCATION/Qualifiers
1..330
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/db_xref='taxon:10118'
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Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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RESULT 14

BD010835 384 bp DNA linear PAT 31-JAN-2002
DEFINITION Novel polypeptide and DNA thereof.
ACCESSION BD010835
VERSION BD010835.1 GI:18639208
KEYWORDS JP 2001069994-A/36.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 384)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 36 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/36
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PI YASUAKI ITO,KAZUNORI NISHI,KAZUHIRO OGI,SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI,KOJI YOSHIMURA,HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
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PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
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FT /organism='Rattus sp. (rat)'.
LOCATION/Qualifiers
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/organism='Rattus sp.'
/db_xref='taxon:10118'
BASE COUNT 98 a 72 c 109 g 105 t
ORIGIN

Query Match 75.5%; Score 249; DB 6; Length 384;
Best Local Similarity 84.8%; Pred. No. 6.1e-64;
Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 1 catggaattttatgacgcgttagcttccaagaagcctctgtgcagatgatagtgctgc 60
Db 55 CATGGCATGTTTATGGATAAACTTTCTTCTTAAGAAAGTTGTGTGCAGATGAGGAGTGTGC 114
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Db 295 TATTTCCCAACCAACTTGGTTAGAGAGCAACGAGTGTACCAGGAGGCCACCAAGGAGATT 354
QY 301 ccaacagcagatattgacttcttctgcga 329
Db 355 CCAACGACGGATATGTGACTTCTTCTGTGA 383

RESULT 15

BD010830
CUS BD010830 307 bp DNA linear PAT 31-JAN-2002
INITIATION Novel polypeptide and DNA thereof.
ACCESSION BD010830
VERSION BD010830.1 GI:18639203
KEYWORDS JP 2001069994-A/31.
SOURCE Rattus sp.
ORGANISM Rattus sp.

REFERENCE 1 (bases 1 to 307)
AUTHORS Ito,Y., Nishi,K., Ogi,K., Okubo,S., Mogi,S., Noguchi,Y.,
Yoshimura,K. and Tanaka,H.
TITLE Novel polypeptide and DNA thereof
JOURNAL Patent: JP 2001069994-A 31 21-MAR-2001;
TAKEDA CHEMICAL INDUSTRIES LTD

COMMENT OS Rattus sp. (rat)
PN JP 2001069994-A/31
PD 21-MAR-2001
PF 29-JUN-2000 JP 2000195911
PR YASUAKI ITO, KAZUNORI NISHI, KAZUHIRO OGI, SHOICHI OKUBO, PI
SHINICHI MOGI,
PI YUKO NOGUCHI, KOJI YOSHIMURA, HIDEYUKI TANAKA
PC C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P9/00,A61P19/02, PC
A61P19/08,
PC C07K14/47,C07K16/18,C12N1/21,C12N5/10,G01N33/15,G01N33/50, PC
G01N33/53//
PC C12P21/08,C12N15/00,A61K37/02,C12N5/00
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PH Key Location/Qualifiers
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FT /organism="Rattus sp. (rat)".
Location/Qualifiers
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FEATURES
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Best Local Similarity 82.1%; Pred. No. 1.2e-53;
Matches 247; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
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Db 7 CATGGTGTATTTATGATAAATCTTCTTCTTAAGAAAGTTGTGTCAGATGAGGAGTGTGTC 66
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Db 67 TATACCATTTCTCTGGCAAGAGACAGAGACTACAAATGCCCGGACTGTAGTTTCATC 126
QY 121 aacgttataaaagggcagcagatctatgttactcaagctgtgtaaaagaaatggagct 180

Db 127 AATGTCGAAGAAAGGCGACAGATCTATGTTTATTCGAAGCTGTGTAACAGAAAATGGAGCT 186
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Db 187 GGGCATTCTGGGCTGGCAGTGTATGGTGACCAACAGGATGAGATGGGAATTGTGGGT 246
QY 241 tatttccccaggaacttgggtcaaggaacagcgtgtgtaccaggaagctaccaggaagt 300
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QY 301 c 301
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 13:38:35 ; Search time 1903.73 Seconds
(without alignments)
2339.615 Million cell updates/sec

Title: US-10-019-455a-23
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Scoring table: IDENTITY_NUC
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Searched: 13736207 seqs, 6748477542 residues

al number of hits satisfying chosen parameters: 27472414

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: em_esthum: *
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4: em_estnu: *
5: em_estov: *
6: em_estpl: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
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12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	190.4	57.7	527	9 BE236443	BE236443 144645 MA
3	157.4	47.7	349	9 AW023324	AW023324 df53d01.y
4	131.6	39.9	338	9 AW021345	AW021345 df21c01.y
5	110	33.3	678	9 BB647928	BB647928 BB647928
6	107.2	32.5	492	9 AA22297	AA22297 mv77b12.r
7	82	24.8	576	10 B1492218	B1492218 df21c01.w
8	64.6	19.6	533	10 W74647	W74647 zd77e05.s1
9	63.4	19.2	373	10 BF691795	BF691795 602248344
10	63.4	19.2	890	10 BG766328	BG766328 602739014
11	63.4	19.2	1140	10 BG765502	BG765502 602739414
12	62.4	18.9	657	12 AG141467	AG141467 Pan trogl
13	61.8	18.7	430	10 BF439750	BF439750 nad13c10.
14	61.8	18.7	442	9 AA282143	AA282143 zt02b05.s
15	61.6	18.7	388	10 BS625492	BS625492 uul19d01.y
16	61.6	18.7	440	9 BB749350	BB749350 BB749350
17	61.6	18.7	464	9 AI323423	AI323423 mj58f08.x

18	61.6	18.7	465	9 AA003262	AA003262 mg51c10.r
19	61.6	18.7	555	10 B1851688	B1851688 603377922
20	61.4	18.6	381	9 AI620915	AI620915 tu05e09.x
21	61.4	18.6	698	10 BE960967	BE960967 601648520
22	61.2	18.5	453	9 AA428926	AA428926 zv77d08.r
23	60.2	18.2	453	9 AA627297	AA627297 nq68g01.s
24	60.2	18.2	457	10 BE864464	BE864464 UI-M-BH1-
25	60	18.2	409	9 AW046043	AW046043 UI-M-BH1-
26	58.8	17.8	496	9 AW444509	AW444509 UI-H-B13-
27	57.4	17.4	425	10 W75984	W75984 zd58e03.r1
28	56.6	17.2	300	9 AU099830	AU099830 AU099830
29	56.4	17.1	396	10 W80195	W80195 me87d07.r1
30	56.4	17.1	475	9 AA982842	AA982842 ub59e03.r
31	55.4	16.8	391	9 AI275598	AI275598 qm48a04.x
32	55.2	16.7	481	9 AI323068	AI323068 mj58f08.y
33	54.2	16.4	437	9 AV592759	AV592759 AV592759
34	54.2	16.4	517	10 BE665724	BE665724 154861 MA
35	53.4	16.2	392	10 W54756	W54756 md10g04.r1
36	53.4	16.2	750	10 BF160660	BF160660 601768554
37	53.2	16.1	448	9 AA537462	AA537462 vk47d10.r
38	53	16.1	767	10 BF977676	BF977676 602147484
39	52.8	16.0	345	9 AW326170	AW326170 18352 MAR
40	52.6	15.9	589	9 AV169321	AV169321 AV169321
41	52.2	15.8	452	9 AA960553	AA960553 ub59e03.s
42	52	15.8	668	10 BF977955	BF977955 602148428
43	51.2	15.5	386	10 W54019	W54019 md09a01.r1
44	50.2	15.2	328	9 AA058045	AA058045 mj58f08.r

ALIGNMENTS

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LOCUS BB611549 RIKEN full-length enriched, 13 days embryo head Mus
DEFINITION musculus cDNA clone 3110083012 5', mRNA sequence.
ACCESSION BB611549
VERSION BB611549.1 GI:15393547
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS I (bases 1 to 696)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayata,J., Muramatsu,M. and Hayashizaki,Y.
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
waqi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Satahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

	/db_xref="taxon:9606" /clone="IMAGE:2484072" /clone_lib="Morton Fetal Cochlea" /tissue_type="cochlea" /dev_stage="16-22 week fetus" /lab_host="SOLR cells (kanamycin resistant)" /note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dT. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' GAATTCGCGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTTTTTTTTT 3"
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Matches	82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	249 caggaacttgctcaaggacagcgtggtaccagaagctaccaaggagtccccaccac 308
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Qy	309 ggattatgactttcttcgcgag 330
Db	516 GGATATTGACTTCTCTGCAG 495
RESULT	8
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LOCUS	W74647.1 GI:1384860
DEFINITION	wz77e05_s1 Soares fetal heart_NbhH19w Homo sapiens CDNA clone IMAGE:346688 3' similar to PIR:S40238 S40238 melanoma-derived growth regulatory protein MIA - human ; , mRNA sequence.
ACCESSION	W74647
VERSION	EST.
KEYWORDS	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 533)
AUTHORS	Hillier,L., Clark,N., Dubucque,T., Elliston,K., Hawkins,M., Holman M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston R., Williamson,A., Wohldmann,P. and Willson,R.
TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilsson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 673 Std Error: 0.00 Seq primer: Etprimer High quality sequence stop: 403. Location/Qualifiers 1..533 /organism="Homo sapiens" /db_xref="GDB:1272063" /db_xref="taxon:9606" /clone="IMAGE:346688" /clone_lib="Soares_fetal_heart_NbhH19w" /sex="unknown" /dev_stage="19 weeks" /lab_host="DH10B (ampicillin resistant)" /note="Organ: heart; Vector: p773D (Pharmacia) with a modified polylinker; Site_1 Not I; Site_2: Eco RI; 1st
FEATURES	source

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BASE COUNT	141 a 96 c 111 g 144 t
ORIGIN	
Query Match	32.5%; Score 107.2; DB 9; Length 492;
Best Local Similarity	86.8%; Pred. No. 2.2e-20;
Matches	118; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Qy	194 ctggcagcttgtatgtgatgccaggacagatggagctcggttatcccccagga 253
Db	1 CTGCGAGTGTATTGTGACCAACACGAGTGCAGATGGGTAATTAGTGTATTTCGCCAGCA 60
Qy	254 acttggtcaaggacagcgtgtaccagaagctaccagaagttccccaccgcgata 313
Db	61 ACTTGTGAAGGAGCAGCGTGTATACAGAGCGCCACCAAGGAGATCCCAACCCGGATA 120
Qy	314 ttgactttcttcgcga 329
Db	121 TTGACTTCTTCTGTGA 136
RESULT	7
BI492218/c	
LOCUS	BI492218.1 GI:15331562
DEFINITION	df2lc01_w1 Morton Fetal Cochlea Homo sapiens CDNA clone IMAGE:2484072 3', mRNA sequence.
ACCESSION	BI492218
VERSION	EST.
KEYWORDS	human.
SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 576)
AUTHORS	Robertson,N.G., Khertarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.
TITLE	Isolation of novel and known genes from a human fetal cochlear CDNA library using subtractive hybridization and differential screening
JOURNAL	Genomics 23, 42-50 (1994)
MEDLINE	95130111
COMMENT	Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996 Email: cmorton@rics.bwh.harvard.edu DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov). This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: L14W6181 row: E column: 1 Seq primer: T7 primer. Location/Qualifiers 1..576 /organism="Homo sapiens"
FEATURES	source


```
LIBRARY
Vector      : pBacE3.6
R.Site 1    : EcoRI
R.Site 2    : EcoRI
Location/Qualifiers
1..657
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J02.7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
201 a 143 c 117 g 189 t 7 others

BASE COUNT      201 a 143 c 117 g 189 t 7 others
ORIGIN
|||||
Query Match      18.9%; Score 62.4; DB 12; Length 657;
Best Local Similarity 98.4%; Pred. No. 2.1e-07;
Matches 63; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 catggaatttcatgacacctagcttccaagaagctctgtgcagatgatgagtgtgc 60
|||||
248 CATGGAATATTTATGACCGCTAGCTTCCAGAGACCTCTGTGCAGATGATGAGTGTCTC 189
Db
QY 61 tata 64
|||
Db 188 TGTA 185

RESULT 13
BF439750/c
LOCUS
DEFINITION
BF439750.1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3365371 3,
similar to SW_MIA_HUMAN Q16674 MELANOMA DERIVED GROWTH REGULATORY
PROTEIN PRECURSOR ;, mRNA sequence.
BF439750
VERSION
BF439750.1 GI:11452267
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 430)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco.
Location/Qualifiers
1..430
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3365371"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids)

FEATURES
source
1..430
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3365371"
/clone_lib="NCI_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/notes="Organ: lung; Vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Plasmid DNA from the normalized
library NCI_CGAP_Lu5 was prepared, and ss circles were
made in vitro. Following HAP purification, this DNA was
used as tracer in a subtractive hybridization reaction.
The driver was PCR-amplified cDNAs from a pool of 5,000
clones made from the same library (clonoids)

1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT      100 a 124 c 125 g 81 t
ORIGIN
|||||
Query Match      18.7%; Score 61.8; DB 10; Length 430;
Best Local Similarity 57.8%; Pred. No. 2.7e-07;
Matches 152; Conservative 0; Mismatches 102; Indels 9; Gaps 2;

QY 12 tatgaccgctagcttccaagaactctgtgcagatgatgagtgtgtctatactatttc 71
|||||
Db 388 TATGCCCAAGTGGGTGACCGGAAGCTGTGTCCGACACAGGAGTGCAGCCACCTATCTC 329
QY 72 tctgctagtgctcaagaagattataatgccccgcgactgtagattcattaaacgtlaaaaa 131
|||||
Db 328 CATGCTGTGGCCCTTCAGGACTACATGTCGCCGACTGCCGATTCCTGTGACCATTCACCG 269
QY 132 agggcagcagatctatgtgtactcaaaagctgtgtataaagaataatggagctggagaattttg 191
|||||
Db 268 GGGCCCAAGTGGGTGATGCTTCTTCCAAGCTG-----AAGGGCCGTGGCGGCTCTTCTCG 215
QY 192 ggtggtgagtggttattgtgtatggtgcagagacagatggag---tcgtgggtatttccc 248
|||||
Db 214 GGGAGGCAGCGTTCAGGGAGATTACTATGGAGATCTGGCTGCTCGCTGGGCTATTTCCC 155
QY 249 caggaacttggtcaaggaacgc 271
|||||
Db 154 CAGTAGCATTTGCCGAGAGGACC 132

RESULT 14
AA282143/c
LOCUS
DEFINITION
AA282143
442 bp mRNA linear EST 14-AUG-1997
Z102B05.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:711921 3,
similar to TR:G438058 G438058 MELANOMA DERIVED GROWTH REGULATORY
PROTEIN MIA PRECURSOR. ;, mRNA sequence.
AA282143
VERSION
AA282143.1 GI:1925022
KEYWORDS
human.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 442)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 1148 Std Error: 0.00
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 337.
Location/Qualifiers
1..442
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:711921"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
/notes="vector: pTT3D-Pac (Pharmacia) with a modified
polylinker; Site:1; Not 1; Site:2; Eco RI; 1st strand cDNA
was prepared from human tonsillar cells enriched for
germinal center B cells by flow sorting (CD20+, IgD-),
provided by Dr. Louis M. Staudt (NCI), Dr. David Allman
(NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was
primed with a Not I - oligo(dT) primer
[5'-TGTTACCAATCTGAAGTGGGAGCGCCCTCATTTTTTTTTTTTTTTT-3'
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2002, 15:36:31 ; Search time 224.07 Seconds
(without alignments)
2528.593 Million cell updates/sec

Title: us-10-019-455a-23

Perfect score: 330

Sequence: 1 catgaatatttgaccg.....atattgactctctgtcgag 330

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

al number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N_Geneseq_032802.*
- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
 - 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
 - 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
 - 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
 - 5: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
 - 6: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
 - 7: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
 - 8: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
 - 9: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
 - 10: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
 - 11: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
 - 12: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1991.DAT.*
 - 13: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1992.DAT.*
 - 14: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
 - 15: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
 - 16: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
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 - 18: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
 - 19: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
 - 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
 - 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
 - 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
 - 23: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
 - 24: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	330	100.0	330	22	AAF59079 Human MLP nucleoti
2	330	100.0	384	22	AAF59065 Human MLP nucleoti
3	330	100.0	387	24	AA517583 DNA encoding novel
4	330	100.0	426	22	AAH26341 Human growth regul
5	330	100.0	891	22	AAH98228 Human EST-derived
6	330	100.0	891	22	AAH26342 Human growth regul
7	330	100.0	923	22	AAF59083 Human MLP nucleoti
8	330	100.0	1201	22	AAH26343 Human growth regul
9	252.2	76.4	330	22	AAF59080 Mouse MLP nucleoti

10	252.2	76.4	384	22	AAF59068	Mouse MLP nucleoti
11	252.2	76.4	947	22	AAF59084	Mouse MLP nucleoti
12	249	75.5	330	22	AAF59099	Rat MLP nucleotide
13	249	75.5	384	22	AAF59098	Rat MLP nucleotide
14	214.6	65.0	307	22	AAF59093	Rat MLP nucleotide
15	193.8	58.7	261	22	AAF59092	Rat MLP nucleotide
16	63.4	19.2	433	22	AAH47783	Recombinant human
17	63.4	19.2	459	16	AAB84050	Sequence encoding
18	63.4	19.2	459	22	AAI70083	Melanoma inhibitor
19	63.4	19.2	459	22	AAI18732	Human antisenase ol
20	63.2	19.2	581	16	AA084052	Sequence encoding
21	57.4	17.4	330	16	AA084061	Amplified fragment
22	54.2	16.4	305	16	AA084055	Human gene express
23	53.6	16.2	300	20	AAZ14828	Human cDNA encodin
24	53.6	16.2	429	22	AA522695	Human cDNA encodin
25	53.6	16.2	884	22	AA522459	Human TANGO 130 cd
26	53.6	16.2	1263	21	AA51245	Human protein enco
27	52	15.8	417	22	AAH99775	Human PRO19670 CDN
28	46	13.9	1060	22	AAH92140	Human DNA encoding
29	46	13.9	1061	22	AA546205	Murine TANGO 130 c
30	46	13.9	2886	21	AAZ51244	Human secreted pro
31	44.2	13.4	421	21	AA03668	Human DNA encoding
32	44.2	13.4	2037	22	AA546220	Sequence encoding
33	40.4	12.2	596	16	AA084066	Sequence encoding
34	40.4	12.2	3565	16	AA084051	Sequence encoding
35	35.6	10.8	13732	24	ABL33820	Human immune syste
36	35	10.6	582	20	AAV86447	EST clone AW728.
37	35	10.6	4292	20	AAH80481	Human secreted pro
38	35	10.6	4292	22	AA59227	Human cDNA encodin
39	35	10.6	4292	24	ABA90896	Human polynucleoti
40	34.4	10.4	2003	23	ABL08217	Drosophila melanog
41	34.4	10.4	6169	23	ABL08216	DNA encoding SNV-e
42	33.8	10.2	1030	22	AAH61509	Recombinant fructo
43	33.6	10.2	1136	17	AAT35254	Tomato LeSNF1 (suc
44	33.6	10.2	1929	22	AAH62011	Endotoxin CryV gen
45	33.6	10.2	2165	18	AAH59702	

ALIGNMENTS

RESULT 1

ID AAF59079 standard; DNA; 330 BP.

AC AAF59079;

XX 23-APR-2001 (first entry)

DT Human MLP nucleotide sequence SEQ ID NO:23.

DE MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

KW cardiant; gene therapy; secretory cell function regulator; promoter;

KW inhibitor; ds.

XX Homo sapiens.

OS WO200102564-A1.

XX 11-JAN-2001.

PD 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

PI Tanaka H;

XX WPI; 2001-159271/16.

XX P-PSDB; AAB69126.

DR


```
XX Homo sapiens.
XX Key Location/Qualifiers
FH 1..387
FT CDS
FT /*tag= a
FT /product= "Human secreted protein"
XX
XX WO200179454-A1.
XX
XX 25-OCT-2001.
XX
XX 11-APR-2001; 2001WO-US11797.
XX
XX 13-APR-2000; 2000US-196603P.
XX 24-APR-2000; 2000US-199417P.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX (SMIK ) SMITHKLINE BEECHAM PLC.
XX
XX Agarwal P, Murdoch PR, Rizvi SK, Smith RF, Xiang Z;
XX
XX WPI; 2002-061975/08.
XX P-PSDB; AAU09871.
XX
XX New secreted proteins or polypeptides, useful for treating e.g. cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, cancer -
XX
XX Claim 2; Page 44; 92pp; English.
XX
XX The invention relates to an isolated novel secreted polypeptide (I) and
XX polynucleotide (II). (I) and (II) are useful for treating cancer,
XX autoimmune diseases, wound healing disorder, infections, haematopoietic
XX disorders, inflammatory disorders, infertility, neurological and
XX psychiatric diseases, cardiovascular diseases, respiratory diseases,
XX renal diseases, or gastrointestinal diseases. These may also be used to
XX treat diseases, abnormalities and disorders caused by abnormal
XX expression, production, function and/or metabolism of the genes, as
XX vaccines for inducing immunological response in a mammal, and in
XX screening methods for detecting the effect of added compounds on the
XX production of mRNA and polypeptide in cells. The polypeptides can be used
XX as immunogens to produce antibodies immunospecific for the polypeptides,
XX and to identify membrane-bound or soluble receptors. The polynucleotides
XX may be used as diagnostic reagents, in chromosome localisation studies,
XX and in tissue expression studies. The present sequence represents the
XX coding sequence of novel human secreted protein #12.
XX
XX Sequence 387 BP; 101 A; 70 C; 106 G; 110 T; 0 other;
XX
XX
XX Query Match 100.0%; Score 330; DB 24; Length 387;
XX Best Local Similarity 100.0%; Pred. No. 3.le-97;
XX Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 catggaattattgacgctgtacgtctccaagaagctctgtgcagatgagtggtc 60
XX |||||
XX DB 55 catggaattattgacgctgtacgtctccaagaagctctgtgcagatgagtggtc 114
XX |||||
XX QY 61 tatactattctctggtctgaagattataatgcccggactgtagattcatt 120
XX |||||
XX DB 115 tatactattctctggtctgaagattataatgcccggactgtagattcatt 174
XX |||||
XX QY 121 aacgttaaaaggcagacagatctatgtgtactcaaaagctgtgtaaaagaatggagct 180
XX |||||
XX DB 175 aacgttaaaaggcagacagatctatgtgtactcaaaagctgtgtaaaagaatggagct 234
XX |||||
XX QY 181 ggagaatttggctggcagtgctttatggtgagccaggacagatgggagctcgtgggt 240
XX |||||
XX DB 235 ggagaatttggctggcagtgctttatggtgagccaggacagatgggagctcgtgggt 294
XX |||||
XX QY 241 tatttccccagactggtcagaagacagctgtgtaccaggaagctaccaagaagtt 300
XX |||||
```

```
Db 295 tatttccccaggaacttggtcaaggaacagcgtgtgtaccaggaagctaccaagaagtt 354
Qy 301 cccaccacggatattgacttcttctgtcgag 330
|||
Db 355 cccaccacggatattgacttcttctgtcgag 384

RESULT 4
AAH26341
ID AAH26341 standard; cDNA; 426 BP.
XX
XX AAH26341;
XX
XX 02-OCT-2001 (first entry)
XX
XX Human growth regulatory-like polypeptide clone 16372272.
XX
XX Growth regulatory-like polypeptide; human; cartilage; melanoma;
XX neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX
XX Homo sapiens.
XX
XX WO200155332-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02455.
XX
XX 25-JAN-2000; 2000US-0491404.
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
XX Drmanac RT;
XX
XX WPI; 2001-483233/52.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders,
XX hyperproliferative disorders, coagulation disorders, and nervous system
XX disorders -
XX
XX Example 1; Page 114; 119pp; English.
XX
XX The present sequence is that of Hyseq clone identification number
XX 16372272, which was obtained from a human thymus cDNA library
XX using standard PCR with primers specific for vector sequence
XX flanking the inserts, sequencing by hybridisation sequence
XX signature analysis, and Sanger sequencing techniques. This
XX expressed sequence tag was used in the assembly of a full-length
XX cDNA sequence (see AAH26343) encoding a novel human growth
XX regulatory-like polypeptide (GRLP, see AAB02671). The GRLP
XX belongs to the same protein family as growth regulatory proteins,
XX growth factors, human melanoma derived growth regulatory protein
XX precursor (64% similarity and 45% identity over 111 amino acids)
XX or melanoma inhibitory activity, cattle cartilage-derived
XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
XX similarity over 126 amino acids) and other retinoic acid-sensitive
XX proteins. GRLP polypeptides and polynucleotides of the invention
XX can be used in the prophylaxis, treatment (including gene therapy)
XX and diagnosis of disorders and diseases caused by, or involving,
XX cartilage development and maintenance, inhibition of melanoma cell
XX growth and tumours, including neuroectodermal tumours such as
XX gliomas. The polynucleotides can also be used to design probes
XX and primers, for chromosome and gene mapping, in the recombinant
XX production of protein, in the generation of antisense, ribozyme and
XX peptide-nucleic acid molecules, and to produce transgenic animals.
XX
XX Sequence 426 BP; 119 A; 73 C; 113 G; 120 T; 1 other;
```

Query Match 100.0%; Score 330; DB 22; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.2e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catggaattatttatggacgcttagcttccaagaagctctgtgcagatgatgagtgtgc 60
DB 73 catggaattatttatggacgcttagcttccaagaagctctgtgcagatgatgagtgtgc 132

QY 61 tatactattctctgctgctcaagaagattataatgcccgactgtagattcatt 120
DB 133 tatactattctctgctgctcaagaagattataatgcccgactgtagattcatt 192

QY 121 aacgttaaaaaaggcagcagatctatgtactcaagctgtgtaaaagaaatggagct 180
DB 193 aacgttaaaaaaggcagcagatctatgtactcaagctgtgtaaaagaaatggagct 252

QY 181 ggagaattttggcctggcagtgcttattggatggccggagcagatgggagctgtgggt 240
DB 253 ggagaattttggcctggcagtgcttattggatggccggagcagatgggagctgtgggt 312

QY 241 tatttccccaggaacttggctcaaggaacagcgtgtgtaccaggaagctaccagaagaatt 300
DB 313 tatttccccaggaacttggctcaaggaacagcgtgtgtaccaggaagctaccagaagaatt 372

QY 301 ccacacaggtattgacttcttctgcgag 330
DB 373 ccacacaggtattgacttcttctgcgag 402

RESULT 5

AAH98228
ID AAH98228 standard; cDNA; 891 BP.
XX AC AAH98228;
XX DT 12-OCT-2001 (first entry)
XX DE Human EST-derived coding sequence SEQ ID NO: 85.
XX KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02687.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 17-JUL-2000; 2000US-0617746.
XX PR 03-AUG-2000; 2000US-0631451.
XX PR 15-SEP-2000; 2000US-0663870.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX DR P-PSDB; AAM23569.
XX PT Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX Claim 1; Page 236; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.

SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 100.0%; Score 330; DB 22; Length 891;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catggaattatttatggacgcttagcttccaagaagctctgtgcagatgatgagtgtgc 60
DB 73 catggaattatttatggacgcttagcttccaagaagctctgtgcagatgatgagtgtgc 132

QY 61 tatactattctctgctgctcaagaagattataatgcccgactgtagattcatt 120
DB 133 tatactattctctgctgctcaagaagattataatgcccgactgtagattcatt 192

QY 121 aacgttaaaaaaggcagcagatctatgtactcaagctgtgtaaaagaaatggagct 180
DB 193 aacgttaaaaaaggcagcagatctatgtactcaagctgtgtaaaagaaatggagct 252

QY 181 ggagaattttggcctggcagtgcttattggatggccggagcagatgggagctgtgggt 240
DB 253 ggagaattttggcctggcagtgcttattggatggccggagcagatgggagctgtgggt 312

QY 241 tatttccccaggaacttggctcaaggaacagcgtgtgtaccaggaagctaccagaagaatt 300
DB 313 tatttccccaggaacttggctcaaggaacagcgtgtgtaccaggaagctaccagaagaatt 372

QY 301 ccacacaggtattgacttcttctgcgag 330
DB 373 ccacacaggtattgacttcttctgcgag 402

RESULT 6

AAH26342
ID AAH26342 standard; cDNA; 891 BP.
XX AC AAH26342;
XX DT 02-OCT-2001 (first entry)
XX DE Human growth regulatory-like polypeptide partial cDNA clone.
XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;
XX ss.
XX OS Homo sapiens.
XX PN WO200155332-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US02455.
XX PR 25-JAN-2000; 2000US-0491404.
XX PR 02-MAY-2000; 2000US-0563786.
XX PA (HYSE-) HYSEQ INC.
XX PI Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX WPI; 2001-483233/52.
XX PT Isolated human growth regulatory-like polypeptide useful for treating
XX e.g. Alzheimer's disease, cancer, autoimmune disorders, and
XX hyperproliferative disorders, coagulation disorders, and nervous system

PT disorders -
XX
PS Claim 1: Page 115; 119pp; English.
XX
CC The present sequence is that of a novel nucleic acid that was
CC assembled from human thymus cDNA library-derived Hyseq clone
CC identification number 16372272 (see AAH26341). A recursive
CC algorithm was used to extend the clone by pulling additional
CC sequences from different databases. A full-length sequence (see
CC AAH26343) encoding novel human growth regulatory-like polypeptide
CC (GRLP, see AAB82671) was subsequently obtained. Human GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor [64% similarity and 45% identity over 111 amino acids]
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polynucleotides can also be used to design probes
CC and primers, for chromosome and gene mapping, in the recombinant
CC production of protein, in the generation of antisense, ribozyme and
CC peptide-nucleic acid molecules, and to produce transgenic animals.
XX
SQ Sequence 891 BP; 272 A; 146 C; 214 G; 259 T; 0 other;

Query Match 100.0%; Score 330; DB 22; Length 891;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catggaattattatgacccgtctagcttccaagaagctctgtgcagatgatggtgtgc 60
DB 73 catggaattattatgacccgtctagcttccaagaagctctgtgcagatgatggtgtgc 132

QY 61 tatactatttctgtgctagctcagaagattataatgcccgcgactgtagattcatt 120
DB 133 tatactatttctgtgctagctcagaagattataatgcccgcgactgtagattcatt 192

QY 121 aacgtttaaaaaaggcagcagatctatgttactcaaaagctgtataaaagaaatggagct 180
DB 193 aacgtttaaaaaaggcagcagatctatgttactcaaaagctgtataaaagaaatggagct 252

QY 181 ggagaattttggcgtgctggtttatggtgagccagacgagatggagtcgtgggt 240
DB 253 ggagaattttggcgtgctggtttatggtgagccagacgagatggagtcgtgggt 312

QY 241 tatttccccaggaacttggtcaaggaaacgctgtgtaccagaaagctaccaggaagt 300
DB 313 tatttccccaggaacttggtcaaggaaacgctgtgtaccagaaagctaccaggaagt 372

QY 301 cccaccacggatattgacttcttcgcgag 330
DB 373 cccaccacggatattgacttcttcgcgag 402

RESULT 7
AAF59083
ID AAF59083 standard; DNA; 923 BP.
XX
AC AAF59083;
XX
XX
DT 23-APR-2001 (first entry)
XX
DE Human MLP nucleotide sequence SEQ ID NO:29.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.

XX Homo sapiens.
XX WO200102564-A1.
XX 11-JAN-2001.
XX 29-JUN-2000; 2000WO-JP04278.
XX 30-JUN-1999; 99JP-0186718.
XX (TAKE) TAKEDA CHEM IND LTD.
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI; 2001-159271/16.
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX Example 1; Page 99-100; 111pp; Japanese.
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
SQ Sequence 923 BP; 303 A; 147 C; 213 G; 260 T; 0 other;

Query Match 100.0%; Score 330; DB 22; Length 923;
Best Local Similarity 100.0%; Pred. No. 4.6e-97;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catggaattattatgacccgtctagcttccaagaagctctgtgcagatgatggtgtgc 60
DB 88 catggaattattatgacccgtctagcttccaagaagctctgtgcagatgatggtgtgc 147

QY 61 tatactatttctgtgctagctcagaagattataatgcccgcgactgtagattcatt 120
DB 148 tatactatttctgtgctagctcagaagattataatgcccgcgactgtagattcatt 207

QY 121 aacgtttaaaaaaggcagcagatctatgttactcaaaagctgtataaaagaaatggagct 180
DB 208 aacgtttaaaaaaggcagcagatctatgttactcaaaagctgtataaaagaaatggagct 267

QY 181 ggagaattttggcgtgctggtttatggtgagccagacgagatggagtcgtgggt 240
DB 268 ggagaattttggcgtgctggtttatggtgagccagacgagatggagtcgtgggt 327

QY 241 tatttccccaggaacttggtcaaggaaacgctgtgtaccagaaagctaccaggaagt 300
DB 328 tatttccccaggaacttggtcaaggaaacgctgtgtaccagaaagctaccaggaagt 387

QY 301 cccaccacggatattgacttcttcgcgag 330
DB 388 cccaccacggatattgacttcttcgcgag 417

RESULT 8
AAH26343
ID AAH26343 standard; cDNA; 1201 BP.
XX
AC AAH26343;
XX
DT 02-OCT-2001 (first entry)

XX DE Human growth regulatory-like polypeptide cDNA.

XX KW Growth regulatory-like polypeptide; human; cartilage; melanoma;

XX KW Neuroectodermal tumour; glioma; cancer; gene therapy; diagnosis;

XX KW ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 33..419

XX FT sig_peptide /*tag= a

XX FT mat_peptide /*tag= b

XX FT /*tag= c

XX WO200115332-A2.

XX PD 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02455.

XX 25-JAN-2000; 2000US-0491404.

XX 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX MIze NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

XX Drmanac RT;

XX WPI; 2001-483233/52.

XX P-PSDB; AAB82671.

XX Isolated human growth regulatory-like polypeptide useful for treating

XX e.g. Alzheimer's disease, cancer, autoimmune disorders, and nervous system

XX hyperproliferative disorders, coagulation disorders, and nervous system

XX disorders -

XX Claim 1; Page 115-116; 119pp; English.

XX The present sequence is that of a novel nucleic acid encoding

XX human growth regulatory-like polypeptide (GRLP, see AAB82671).

XX The sequence was assembled using human thymus cDNA library-derived

XX Hyseq clone identification number 16372272 (see AAB82671) as seed,

XX using software programs to pull additional sequences from Hyseq's

XX proprietary database containing expressed sequence tag sequences,

XX and by gel sequencing using primers to extend both 5' and 3' ends.

XX The predicted protein has a mol.wt. of 14 kDa unglycosylated. GRLP

XX belongs to the same protein family as growth regulatory proteins,

XX growth factors, human melanoma derived growth regulatory protein

XX precursor (64% similarity and 45% identity over 111 amino acids)

XX or melanoma inhibitory activity, cattle cartilage-derived

XX retinoic acid sensitive protein (CD-RAP, 44% identity and 64%

XX similarity over 126 amino acids) and other retinoic acid-sensitive

XX proteins. GRLP polypeptides and polynucleotides of the invention

XX can be used in the prophylaxis, treatment (including gene therapy)

XX and diagnosis of disorders and diseases caused by, or involving,

XX cartilage development and maintenance, inhibition of melanoma cell

XX growth and tumours, including neuroectodermal tumours such as

XX gliomas. The polynucleotides can also be used to design probes

XX and primers, for chromosome and gene mapping, in the recombinant

XX production of protein, in the generation of antisense, ribozyme and

XX peptide-nucleic acid molecules, and to produce transgenic animals.

XX They may also have cytokine and cell proliferation or

XX differentiation activity, stem cell growth factor activity,

XX haematopoiesis regulating activity, tissue growth activity,

XX immunosuppressive or immunostimulant activity, activin/inhibin

XX activity, chemotactic/chemokinetic activity, haemostatic and

XX thrombolytic activity, use in cancer diagnosis and therapy,

XX drug screening, receptor/ligand activity, antiinflammatory

XX activity, and treatment of leukaemia, nervous system disorders,

XX arthritis and inflammation.

XX SQ Sequence 1201 BP; 357 A; 188 C; 275 G; 381 T; 0 other;

Query Match 100.0%; Score 330; DB 22; Length 1201;

Best Local Similarity 100.0%; Pred. No. 5.1e-97;

Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 catgaataattatggaccgtctagctccaagaagctctgtgcagatgaatgagtgctc 60

DB 87 catggaataattatggaccgtctagctccaagaagctctgtgcagatgaatgagtgctc 146

QY 61 tatactatttctctgctagctcaagaagattataatgccccgactgtagattcatt 120

DB 147 tatactatttctctgctagctcaagaagattataatgccccgactgtagattcatt 206

QY 121 aacgttaaaaaaggcgagcagatctatgttactcaaaagctggtataaagaatgagct 180

DB 207 aacgttaaaaaaggcgagcagatctatgttactcaaaagctggtataaagaatgagct 266

QY 181 ggagaattttggctggcagtggtttatgtgctgagcagagagatggagtcgtgggt 240

DB 267 ggagaattttggctggcagtggtttatgtgctgagcagagagatggagtcgtgggt 326

QY 241 tatttccccagggaacttggtcaaggaacagcgtgtgtaccaggaaagctaccagggaagt 300

DB 327 tatttccccagggaacttggtcaaggaacagcgtgtgtaccaggaaagctaccagggaagt 386

QY 301 cccaccacggtatgacttcttctgcgag 330

DB 387 cccaccacggtatgacttcttctgcgag 416

RESULT 9

AAF59080

ID AAF59080 standard; DNA; 330 BP.

XX AC AAF59080;

XX DT 23-APR-2001 (first entry)

XX DE Mouse MLP nucleotide sequence SEQ ID NO:25.

XX KW MLP; MTA; melanoma inhibitory activity; cancer; bone disease;

XX KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;

XX KW cardiant; gene therapy; secretory cell function regulator; promoter;

XX KW inhibitor; ds.

XX OS Mus musculus.

XX PN WO200102564-A1.

XX PD 11-JAN-2001.

XX PF 29-JUN-2000; 2000WO-JP04278.

XX PR 30-JUN-1999; 99JP-0186718.

XX PA (TAKE) TAKEDA CHEM IND LTD.

XX PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;

XX PI Tanaka H;

XX DR WPI; 2001-159271/16.

XX DR P-PSDB; AAB69127.

XX Safe, low-toxicity secretory cell function-regulatory protein and

XX PT encoded DNA, applicable as drugs, in diagnosis and development of

XX PT promoters and inhibitors for preventing or treating e.g. bone and joint

XX PT diseases -

XX PS Claim 10; Page 98; 111pp; Japanese.

XX

CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 330 BP; 91 A; 60 C; 92 G; 87 T; 0 other;

Query Match 76.4%; Score 252.2; DB 22; Length 330;
Best Local Similarity 85.4%; Pred. No. 5.7e-72;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 catggaattatttgaccgcttagcttccaaagaagattataatgccccgactgtagattcatt 60
DB 1 catggtgtatttgataaaactttcttaagaagttgtgctgagatgagagtgctc 60
DB 61 tatactatttctctggctagtgctcaagaagattataatgccccgactgtagattcatt 120
QY 121 aacgttaaaaaaggcagcagatctatgttactcaaaactgtgtaaaagaatggagct 180
DB 121 gatgtcaagaaggcagcagatctatgttactcaaaactgtgtaaaagaatggagct 180
QY 181 ggagaattttggctgctgagtgcttattgtatggcagcagagatggagctgggt 240
DB 181 ggagaattttggctgctgagtgcttattgtatggcagcagagatggagctgggt 240
QY 241 tatttccccaggaacttggtcaaggaaacagcggtgtgtaccaggaagctaccagggaagt 300
DB 241 tatttccccaggaacttggtgaaggagcagcggtgtataccaggaggcccaaggagatc 300
QY 301 ccacacacgagattgactttcttcgca 329
DB 301 ccaacacgagattgactttcttcgta 329

RESULT 10
AAF59068
ID AAF59068 standard; DNA; 384 BP.
XX
AC AAF59068;
XX
23-APR-2001 (first entry)

Mouse MLP nucleotide sequence SEQ ID NO:10.
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
OS Mus musculus.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI; 2001-159271/16.
DR P-PSDB; AAB69125.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
XX Claim 11; Page 93; 111pp; Japanese.
PS
CC The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.
XX
SQ Sequence 384 BP; 98 A; 68 C; 111 G; 107 T; 0 other;

Query Match 76.4%; Score 252.2; DB 22; Length 384;
Best Local Similarity 85.4%; Pred. No. 6.1e-72;
Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 1 catggaattatttgaccgcttagcttccaaagaagctctgtgcagatgatgagtgctc 60
DB 55 catggtgtatttgataaaactttcttaagaagttgtgctgagatgagagtgctc 114
QY 61 tatactatttctctggctagtgctcaagaagattataatgccccgactgtagattcatt 120
DB 115 tatactatttctctggcagagacaggaagattataatgccccgactgtagattcatt 174
QY 121 aacgttaaaaaaggcagcagatctatgttactcaaaactgtgtaaaagaatggagct 180
DB 175 gatgtcaagaaggcagcagatctatgttactcaaaactgtgtaaaagaatggagct 234
QY 181 ggagaattttggctgctgagtgcttattgtatggcagcagagatggagctgggt 240
DB 235 ggagaattttggctgctgagtgcttattgtatggcagcagagatggagctgggt 294
QY 241 tatttccccaggaacttggtcaaggaaacagcggtgtgtaccaggaagctaccagggaagt 300
DB 295 tatttccccaggaacttggtgaaggagcagcggtgtataccaggaggcccaaggagatc 354
QY 301 ccacacacgagattgactttcttcgca 329
DB 355 ccaacacgagattgactttcttcgta 383

RESULT 11
AAF59084
ID AAF59084 standard; DNA; 947 BP.
XX
AC AAF59084;
XX
DT 23-APR-2001 (first entry)
XX
DE Mouse MLP nucleotide sequence SEQ ID NO:30.
XX
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
OS Mus musculus.
XX
PN WO200102564-A1.
XX
PD 11-JAN-2001.
XX
PF 29-JUN-2000; 2000WO-JP04278.
XX
PR 30-JUN-1999; 99JP-0186718.

```

XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX WPI: 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Example 2; Page 100-101; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 947 BP; 279 A; 158 C; 221 G; 289 T; 0 other;
XX
XX
XX Query Match 76.4%; Score 252.2; DB 22; Length 947;
XX Best Local Similarity 85.4%; Pred. No. 9.2e-72;
XX Matches 281; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
XX
XX QY 1 catggaattttatgaccgtctagcttccaagaagctctgtgcagatgatgagtgtgc 60
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 65 catggtgtattatggataaaactttcttctaagaagtgtgtgcgagtgaggagtgtgc 124
XX
XX QY 61 tatactatttcttgctgactgctcaagaagattataatgccccgactgtagattcatt 120
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 125 tatactatttcttgccaagagcacaggaagtattacaatgccacagactgtaggttcac 184
XX
XX QY 121 aacgttaaaaaaggcagcagatctatgttactcaaaagctggttaaaagaatggagct 180
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 185 gatgtcaagaagaaggcagcagatctatgtttactccaagctggttaacagaacaggagct 244
XX
XX QY 181 ggagaattttggctggcagtggtttatgtgatggccagacagagatgggagtcgtgggt 240
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 245 ggagagttttggctggcagtggtttatgttgaccaccaggatgagatgggaaattgtaggt 304
XX
XX QY 241 tatttccccaggaactgttcaagaaacagcgtgtgtaccaggaagctaccaggaagtt 300
XX b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 305 tatttccccagcaactgttgaggagcggtgtataccadgagggccaccagagagatc 364
XX
XX QY 301 cccaccacggatattgacttcttctgcga 329
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 365 ccaaccacggatattgacttcttctgcga 393
XX
XX RESULT 12
XX AAF59099
XX ID AAF59099 standard; DNA; 330 BP.
XX
XX AC AAF59099;
XX
XX XX
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP nucleotide sequence SEQ ID NO:48.
XX
XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX OS Rattus sp.,
XX

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PN W0200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX WPI: 2001-159271/16.
XX
XX P-PSDB; AAB69131.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases -
XX
XX Claim 12; Page 107; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 330 BP; 91 A; 62 C; 91 G; 86 T; 0 other;
XX
XX
XX Query Match 75.5%; Score 249; DB 22; Length 330;
XX Best Local Similarity 84.8%; Pred. No. 6.2e-71;
XX Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
XX
XX QY 1 catggaattttatgaccgtctagcttccaagaagctctgtgcagatgatgagtgtgc 60
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 1 catggtcatgtttatggataaaactttcttctaagaagtgtgtgcagatgaggagtgtgc 60
XX
XX QY 61 tatactatttcttgctgactgctcaagaagattataatgccccgactgtagattcatt 120
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 61 tataccatttcttgccaagagcacaggaagtataatgccccgactgtaggttcac 120
XX
XX QY 121 aacgttaaaaaaggcagcagatctatgttactcaaaagctggttaaaagaatggagct 180
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 121 aatgtcaagaagaaggcagcagatctatgtttattccaagctggttaacagaacaggagct 180
XX
XX QY 181 ggagaattttggctggcagtggtttatgtgatggccagacagagatgggagtcgtgggt 240
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 181 ggaggatcttctggctggcagtggtttatgttgaccaccaggatgagatgggaaattgtggtc 240
XX
XX QY 241 tatttccccaggaactgttcaagaaacagcgtgtgtaccaggaagctaccaggaagtt 300
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 241 tatttccccagcaactgttgaggagcaacgagtgtaggtaccaggaaggccaccaggaagatt 300
XX
XX QY 301 cccaccacggatattgacttcttctgcga 329
XX Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
XX 301 ccaaccacggatattgacttcttctgcga 329
XX
XX RESULT 13
XX AAF59098
XX ID AAF59098 standard; DNA; 384 BP.
XX
XX AC AAF59098;
XX
XX XX
XX DT 23-APR-2001 (first entry)
XX DE Rat MLP nucleotide sequence SEQ ID NO:46.
XX

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```
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.
XX
OS Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX P-PSDB; AAB69130.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases
XX
XX Claim 13; Page 105-106; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 384 BP; 98 A; 72 C; 109 G; 105 T; 0 other;
XX
XX
XX Query Match 75.5%; Score 249; DB 22; Length 384;
XX Best Local Similarity 84.8%; Pred. No. 6.7e-71;
XX Matches 279; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
XX
XX 1 catggaattatttgaccgctctagcttccaagaagctctgtgcagatgatgagtgctc 60
XX ||||| || ||||| || ||||| || ||||| || ||||| || ||||| || |||||
XX 55 catggcatgtttatgataaactttcttctaagaagtgtgtgcagatgagagtgctc 114
XX
XX 61 tatactatttcttggtgctgctcaagaagattataatgcccggactgtagattcatt 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 115 tatactatttcttggtgctgctcaagaagattataatgcccggactgtagattcatt 174
XX
XX 121 aacgtttaaaaggccagcagatctatgttactcaaaagctgtaaaagaaatgagct 180
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 175 aatgtcaaaaggccagcagatctatgttactcaaaagctgtaaaagaaatgagct 234
XX
XX 181 ggagaattttggctggcagtgctttatgtgatggccagacagatggagtcgtgggt 240
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 235 ggagcatcttggtggcagtgctttatgttgaccacacagatgagatgggaattgtgggt 294
XX
XX 241 tatttccccaggaacttgctcaaggacacagctgtgtaccaggaagctaccaggaagtt 300
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 295 tatttccccagcaacttggttagagacacacagctgtaccagagggccaccaaaggagatt 354
XX
XX 301 ccaacacagcatattgacttcttctcga 329
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 355 ccaacacagcatattgacttcttcttga 383
XX
XX RESULT 14
```

```
AAF59093
ID AAF59093 standard; DNA; 307 BP.
XX
XX AAF59093;
XX AC
XX
XX 23-APR-2001 (first entry)
XX
XX Rat MLP nucleotide sequence SEQ ID NO:41.
XX
XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor; ds.
XX
XX OS Rattus sp.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE ) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
XX
XX WPI; 2001-159271/16.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
XX promoters and inhibitors for preventing or treating e.g. bone and joint
XX diseases
XX
XX Example 9; Page 104; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
XX DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
XX activities, and can be used in gene therapy and as secretory cell
XX function regulators. The MLP proteins and DNAs can be used in drugs, in
XX the diagnosis and development of promoters and inhibitors for preventing
XX or treating bone and joint diseases as well as pathologic angiogenesis.
XX AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
XX
XX Sequence 307 BP; 84 A; 56 C; 90 G; 77 T; 0 other;
XX
XX
XX Query Match 65.0%; Score 214.6; DB 22; Length 307;
XX Best Local Similarity 82.1%; Pred. No. 9.3e-60;
XX Matches 247; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
XX
XX 1 catggaattatttgaccgctctagcttccaagaagctctgtgcagatgatgagtgctc 60
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 7 catgggtatttatgataaactttcttctaagaagtgtgtgcagatgagagtgctc 66
XX
XX 61 tatactatttcttggtgctgctcaagaagattataatgcccggactgtagattcatt 120
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 67 tatactatttcttggtgctgctcaagaagattataatgcccggactgtagattcatt 126
XX
XX 121 aacgtttaaaaggccagcagatctatgttactcaaaagctgtaaaagaaatgagct 180
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 127 aatgtcaaaaggccagcagatctatgttactcaaaagctgtaaaagaaatgagct 186
XX
XX 181 ggagaattttggctggcagtgctttatgtgatggccagacagatggagtcgtgggt 240
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 187 ggagcatcttggtggcagtgctttatgttgaccacacagatgagatgggaattgtgggt 246
XX
XX 241 tatttccccaggaacttgctcaaggacacagctgtgtaccaggaagctaccaggaagtt 300
XX ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
XX 247 tatttccccagcaacttggttagagacacacagatgataccagagggccaccaaaggagat 306
```

QY 301 c 301
|
Db 307 c 307

RESULT 15
AAF59092
ID AAF59092 standard; DNA; 261 BP.

XX AAF59092;

AC AAF59092;

DT 23-APR-2001 (first entry)

XX Rat MLP nucleotide sequence SEQ ID NO:40.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor; ds.

XX Rattus sp.

XX WO200102564-A1.

PN 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;

XX WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases

XX Example 9; Page 104; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 261 BP; 72 A; 46 C; 75 G; 68 T; 0 other;

Query Match 58.7%; Score 193.8; DB 22; Length 261;
Best Local Similarity 83.9%; Pred. No. 5e-53;
Matches 219; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 15 ggaccgtctagcttccaaagaactctgtgcagatgatgagtggtctatactattctct 74
Db 1 ggataaactttcttcaagaagtgtgtgcagatgaggagtggtctatactattctct 60

QY 75 ggctagtgtcctaagaattataatgcccgactgtagattcattcaacgttaaaaaagg 134
Db 61 ggcaagagcacaggaagactacaatgcccgactgtagtttcaatcattgtcaaaaaagg 120

QY 135 gcagcagatctatgtgtactaaagctgtgtaaaagaaatggagctggagaattttgggc 194
Db 121 gcagcagatctatgtttattccaagctgttaacagaaaaatggagctgggcatttctgggc 180

QY 195 tggcagtggtttatgggtgatggccagacgagatgggagtcgtgggttatttccccaggaa 254
|
Db 181 tggcagtggtttatgggtgatggccagacgagatgggagtcgtgggttatttccccaggaa 240
QY 255 cttgtcaagggaacagcgtgt 275
|
Db 241 cttgttagagagcaacgagt 261

Search completed: September 23, 2002, 15:55:37
Job time: 1146 sec

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EMBO J. 6, 2263-2270, 1989

Oncogene 7, 611-618, 1992

A;Title: The hematopoietically expressed vav proto-oncogene shares homology with the A;Reference number: S23669; MUID:92228488

C;Keywords: phosphoprotein; transforming protein; zinc finger

C;Accession: I51940

A;Contents: annotation: the authors note the frameshift difference with sequence in A;Note: the complete sequence was submitted to Genbank; see S36941

C;Genetics:

A;Gene: vav

C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding

F;32-102/Region: leucine-rich

F;132-176/Region: acidic

F;194-458/Domain: CDC24 homology <CD24>

F;336-340/Region: proline-rich

F;486-493/Region: nuclear location signal

F;515-563/Domain: protein kinase C zinc-binding repeat homology <K21>

F;528-548/Region: zinc finger CCCC motif

F;553-566/Region: zinc finger HCCH motif

F;575-582/Region: nuclear location signal

F;604-654/Domain: SH3 homology <SH3A>

F;606-609/Region: proline-rich

F;670-761/Domain: SH2 homology <SH2>

F;788-836/Domain: SH3 homology <SH3B>

F;439/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 14.5%; Score 85.5; DB 1; Length 844;
Best Local Similarity 31.4%; Pred. No. 0.86;
Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps 3;

QY 26 ASAQEDYNAPDCRFNVKKGQQIIVYVSKLVKENGAGFEWAGSVYGDQDEMGVVGYFPRN 85
| | | | | : | | | | | : | | | | | : | | | | |
DB 786 AKARYDFPCARDSELSLKEGDII----KILNKGGQGQWRGEIYGR-----IGWFPSN 834
| | | | | : | | | | | : | | | | | : | | | | |

QY 86 LVKEORVYQE 95
| | | | |

DB 835 YVEED--YSE 842
| | | | |

RESULT 4
I51940
gene VAV2 protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C;Accession: I51940
R;Henske, E.P.; Short, M.P.; Jozwiak, S.; Bovey, C.M.; Ramlakhan, S.; Haines, J.L.; K
Ann. Hum. Genet. 59, 25-37, 1995
A;Title: Identification of VAV2 on 9q34 and its exclusion as the tuberous sclerosis g
A;Reference number: I51940; MUID:95283235
A;Accession: I51940
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-878 <RES>
A;Cross-references: GB:S76992; NID:g913345; PIDN:AAB34377.1; PID:g913346
C;Genetics:
A;Gene: GDB:VAV2
A;Cross-references: GDB:370880; OMIM:600428
A;Map position: 9q34-q34
C;Superfamily: vav transforming protein; CDC24 homology; protein kinase C zinc-binding
F;198-462/Domain: CDC24 homology <CD24>
F;524-572/Domain: protein kinase C zinc-binding repeat homology <K22>
F;673-764/Domain: SH2 homology <SH2>
F;823-872/Domain: SH3 homology <SH3>

Query Match 13.8%; Score 81.5; DB 2; Length 878;
Best Local Similarity 26.3%; Pred. No. 2.3;
Matches 20; Conservative 21; Mismatches 22; Indels 13; Gaps 3;

QY 20 VYT---ISLASAEADYNAPDCRFNVKKGQQIIVYVSKLVKENGAGFEWAGSVYGDQDEM 76
| | | | | : | | | | | : | | | | | : | | | | |
DB 812 VFTRPVJGTAVRYFAARMDRELSUREGDVVRYSRIIGDQG---WMKG-----ETN 861
| | | | | : | | | | | : | | | | | : | | | | |

QY 77 GVVGYPFRNLVKEOEV 92

RESULT 12

C90186
AAA family ATPase [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001
C:Accession: C90186
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aweez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90186
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-769 <KUR>
A:Cross-References: GB:AE006641; NID:gl13813572; PIDN:AAK40746.1; GSPDB:GN00155
C:Genetics:
A:Gene: SSO0421
Superfamily: transitional endoplasmic reticulum ATPase; FtsH/SEC18/CDC48-type ATP-bind

Query Match 12.0%; Score 71; DB 2; Length 769;
Best Local Similarity 35.0%; Pred. No. 25;
Matches 28; Conservative 10; Mismatches 20; Indels 22; Gaps 5;
QY 49 YVSKLVKNG-----AGFEWAGSVYGDG--QDEMGVGVYFPRNL-----VKE 89
DB 51 YTISRIGIENGDIYVEIGPSGALAQALIGDIADNEIRVDGIYRIRSGVIGIGDEVTVKR 110
QY 90 ORVYOATKEV--PTTDIDF 107
DB 111 AQV-QDATKVVLAPQISF 129

RESULT 13

D72278
endo-1,4-beta-mannosidase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316
C:Accession: D72278
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-669 <ARN>
A:Cross-References: GB:AE001779; GB:AE000512; NID:g4981777; PIDN:AAD36302.1; PID:g498178
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1227

Query Match 11.9%; Score 70.5; DB 2; Length 669;
Best Local Similarity 27.6%; Pred. No. 24;
Matches 32; Conservative 12; Mismatches 37; Indels 35; Gaps 6;
QY 25 LASAQEDYNAPDCRFINVKKGQOI-----YVYSK-----LVKENCAGEF 63
DB 393 LFTGTGDIREDTCSFLPLKDGMEIKTVEVRAGVFDYSNTEKLSVKYEDLVFENEIHL 452
QY 64 WAGSVYV-----DGDGEMGVGVYFPRNLVKEQ---RVYOATKEVPTTDIDF 107
DB 453 GYG-IGFPLDTRTPDGEHEMFEGHFGCKTVKSIKAKVVNEA-RYVLAEEVD 506

RESULT 14

D86758
orotate phosphoribosyltransferase (EC 2.4.2.10) [imported] - Lactococcus lactis subsp.

C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: D86758
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Eh
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86758
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-209 <STO>
A:Cross-References: GB:AE005176; PID:gl12724022; PIDN:AAK05166.1; GSPDB:GN00146
A:Experimental source: strain ILL403
C:Genetics:
A:Gene: pyrE
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 11.9%; Score 70; DB 2; Length 209;
Best Local Similarity 26.9%; Pred. No. 7.7;
Matches 21; Conservative 15; Mismatches 42; Indels 0; Gaps 0;
QY 25 LASAQEDYNAPDCRFINVKKGQOIYVYKLVKENGAGFEWAGSVYGDGEMGVYGFPR 84
DB 95 IRSPKPDHGAGNQVEGRVTGQKMWVVEDLISTGGSVLEAVAAAREGADVLGVVAIFTY 154
QY 85 NLVKQQRVYOATKEVPT 102
DB 155 ELEKANRKFADAGVKLAT 172

RESULT 15

F90113
cell division cycle 2 homolog [imported] - Guillardia theta nucleomorph
C:Species: nucleomorph Guillardia theta
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C:Accession: F90113
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.;
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A99082; MUID:11323671
A:Accession: F90113
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-295 <DOU>
A:Cross-References: GB:AJ010592; NID:gl2580757; PIDN:CAC27075.1; GSPDB:GN00151
C:Genetics:
A:Map position: 2
A:Genome: nucleomorph
C:Superfamily: Kinase-related transforming protein; protein kinase homology
C:Keywords: nucleomorph

Query Match 11.8%; Score 69.5; DB 2; Length 295;
Best Local Similarity 28.0%; Pred. No. 13;
Matches 28; Conservative 14; Mismatches 31; Indels 27; Gaps 6;
QY 8 LASKKLCADECVYTITSLASQAQEDYNAPDCRFINVKKGQOIYVYKLVKENGAG--GEFWA 65
DB 157 LCSKKICLSKIV-TLW-----YRAPE-----ILLGQHFYDYSVDWMSFGCVIGELIT 203
QY 66 GSVYGDGQDEMGVGVYFPRNLVKEQRYOATKEVPTTDI 105
DB 204 GEILFOGKSELQDL-----NKIFO--TIGTPTTEI 231

Search completed: September 23, 2002, 09:37:17
Job time: 27 sec

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	226.5	38.4	96	11	Q9J109	Q9J109 mesocricetu	
2	185.5	31.4	119	4	Q96PC5	Q96PC5 homo sapien	
3	181	30.7	137	11	Q921X3	Q921X3 mus musculus	
4	171.5	29.1	119	11	Q91ZV0	Q91ZV0 mus musculus	
5	168.5	28.6	88	13	Q90XF1	Q90XF1 tetraodon n	
6	88.5	15.0	1196	4	Q9HOH2	Q9HOH2 homo sapien	
7	86.5	14.7	719	4	Q96D37	Q96D37 homo sapien	
8	85.5	14.5	166	11	Q08526	Q08526 mus musculus	
9	82.5	14.0	498	4	Q9H803	Q9H803 homo sapien	
10	77	13.1	331	2	Q93J77	Q93J77 pseudomonas	
11	74.5	12.6	1215	5	Q77202	Q77202 acanthamoeb	
12	74	12.5	308	10	Q9LXG4	Q9LXG4 arabidopsis	
13	74	12.5	2161	4	Q9Y366	Q9Y366 homo sapien	
14	73	12.4	636	10	Q9FTZ8	Q9FTZ8 oryza sativ	
15	73	12.4	643	10	Q9FU04	Q9FU04 oryza sativ	
16	72	12.2	344	10	Q9FU07	Q9FU07 oryza sativ	

Qy 64 WAGSV 68
Db 63 WAGSV 87

QY 80 GYFPRNLVKEQRVVQEATKEVP TTDIDFFC 109
| : | | : | | : | | : | | : |
Db 59 GHFPSSIVEETHPLMAAQTEVKTSNWD FYC 88

RESULT 6

SQ SEQUENCE 719 AA; 83727 MW; A51B757DA543BA6C CRC64;
 Query Match 14.7%; Score 86.5; DB 4; Length 719;
 Best Local Similarity 32.9%; Pred. No. 0.5;
 Matches 23; Conservative 13; Mismatches . 21; Indels 13; Gaps
 Qy 26 ASAOEDYNAPDCRFNVKKGQIQIYVYVKLVKENGAGFEWAGSVYGDQDEMVGWYGFPRN 85
 Db 661 AKARYDFCARDRSELSLKEGDII----KILNKKGQGWWRGEIYGR-----VGWFPAN 709
 Qy 86 LVKEQRYQZE 95
 Db 710 YVEED--YSE 717
 RESULT 8
 O08526 PRELIMINARY; PRT; 166 AA.
 AC O08526;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE VAV-T.
 GN VAV.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DDY; TISSUE-TESTIS;
 RX MEDLINE=97190224; PubMed=9038379;
 RA Okumura K., Kaneko Y., Nonoguchi K., Nishiyama H., Yokoi H.,
 RA Higuchi T., Itoh K., Yoshida O., Miki T., Fujita J.;
 RT "Expression of a novel isoform of Vav, Vav-T, containing a single
 RT Src-homology 3 domain in murine testicular germ cells.";
 RL Oncogene 14:713-720(1997).
 DR EMBL; D83266; BAA18950.1; -.
 DR HSP; Q60631; ICBQ.
 DR MGD; MGI:98923; Vav.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR PROSITE; PS00001; SH2; 1.
 DR PROSITE; PS00002; SH3; 1.
 SQ SEQUENCE 166 AA; 19434 MW; 2C3AF1FF07A5018F CRC64;
 Query Match 14.5%; Score 85.5; DB 11; Length 166;
 Best Local Similarity 31.4%; Pred. No. 0.1;
 Matches 22; Conservative 14; Mismatches 21; Indels 13; Gaps
 Qy 26 ASAOEDYNAPDCRFNVKKGQIQIYVYVKLVKENGAGFEWAGSVYGDQDEMVGWYGFPRN 85
 Db 108 AKARYDFCARDRSELSLKEGDII----KILNKKGQGWWRGEIYGR-----IGWFPN 709
 Qy 86 LVKEQRYQZE 95
 Db 157 YVEED--YSE 164
 RESULT 9
 Q09H803 PRELIMINARY; PRT; 498 AA.
 AC Q09H803;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE HYPOTHETICAL 57.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EMBRYO;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugeno S., Shiratori A., Sudo H.,
RA Takatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.,
RT "NEO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AK024085; BAB14820.1; -.
DR HBB; P06241; 1SHF.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR001452; SH3.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00400; WD40; 4.
DR PRINTS; PR00320; GPROTEINBRPT.
DR PRINTS; PR00452; SH3DOMAIN.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00320; WD40; 5.
DR PROSITE; PS50002; SH3; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; UNKNOWN_1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD repeat.
SQ SEQUENCE 498 AA; 57011 MW; 0D2F58A28A4553AC CRC64;

Query Match 14.0%; Score 82.5; DB 4; Length 498;
Best Local Similarity 32.1%; Pred. No. 0.89;
Matches 26; Conservative 12; Mismatches 32; Indels 11; Gaps 4;

QY 20 VYTISSAQEDYNAPDCRFINVKKGQIYVYSLKLVKENGAGFEWAGSVYGDQDMGVV 79
Db 404 VDTAPTVVALDYTNRSDELIRHGDIIRVF---FKDN--EDWYVGSIGKQE----- 452

QY 80 GYFPRNLVKRQYQATKEV 100
Db 453 GYLPANHVASETLYQELPPEI 473

RESULT 10
Q93JT7 PRELIMINARY; PRT; 331 AA.
AC Q93JT7;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DE PROBABLE C4 DICARBOXYLATE BINDING PROTEIN.
GN DCTP.
OS Pseudomonas stutzeri (Pseudomonas perfectomarina).
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=316;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A15;
RA Lin M., Gao L., Desnoes N., Elmerich C.;
RT "Dicarboxylic acid transport in Pseudomonas stutzeri."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ313422; CAC44171.1; -.
SQ SEQUENCE 331 AA; 36729 MW; CB893C98508BEC39 CRC64;

Query Match 13.1%; Score 77; DB 2; Length 331;
Best Local Similarity 25.6%; Pred. No. 2.2;
Matches 30; Conservative 22; Mismatches 43; Indels 22; Gaps 5;

QY 5 MDRLASKKLCADECVYTISLASAQEDYNAPDCRFI-----NVKKGQIYVYSLKLVKENG 59
Db 1 MFKLTAkala----CALSLSIAGLAHADPITIKFSHVVAENTPKGGALMFKKLVEERL 56

QY 60 AGE-----FWAGSVYGDGODE-----MGVYGYPRNLVKEORVYQAEKVEPTTIDIF 107
Db 57 AGKVEQVYVPSNLSFGDGKREMEALLGLDYLTAAPSLAK-----FEHYSKGVQVFDLPF 109

RESULT 11
O77202 PRELIMINARY; PRT; 1215 AA.
AC O77202;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE MYOSIN-IA.
GN MIA.
OS Acanthamoeba castellanii (Amoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEEP;
RA Lee W.-L., Ostap E.M., Zot H.G., Pollard T.D.;
RT "Hydrodynamic and ligand binding properties of Acanthamoeba Myosin-IA
GPA/SH3 domain."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF085185; AAC35357.1; -.
DR HSP; P08799; 1MND.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR001452; SH3.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF00018; SH3; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRODOM; PD000355; myosin_head; 1.
DR SMART; SM00242; MYSC; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS50002; SH3; 1.
SQ SEQUENCE 1215 AA; 134103 MW; FEFBFCC2EF936C72 CRC64;

Query Match 12.6%; Score 74.5; DB 5; Length 1215;
Best Local Similarity 28.6%; Pred. No. 21;
Matches 20; Conservative 12; Mismatches 25; Indels 13; Gaps 2;

QY 20 VYTISSAQEDYNAPDCRFINVKKGQIYVYSLKLVKENGAGFEWAGSVYGDQDMGVV 79
Db 1158 VPTVGRCRALYDYGAEDELTLREGDVIDVIOK-----SGEWWEGLNGK-----T 1204

QY 80 GYFPRNLVKE 89
Db 1205 GVFPANYVED 1214

RESULT 12
Q9LYG4 PRELIMINARY; PRT; 308 AA.
AC Q9LYG4;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DE HYPOTHETICAL 34.0 KDA PROTEIN.
GN T22P22_50.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

```

QY      88 KEQRYVQEATKEVPTTD 104
Db      609 EEVANRSQESKQESRSD 625

RESULT 14
ID Q9FTZ8 PRELIMINARY; PRT; 636 AA.
AC Q9FTZ8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.32 OR P0494A10.10.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
ON NCBI_Taxid=4530;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
RT clone: P0698G03.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RC Sasaki T., Matsumoto T., Yamamoto K.;
RA "Oryza sativa nipponebare(GA3) genomic DNA, chromosome 1, PAC
RT clone: P0494A10.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002747; BAB17348.1; -.
DR EMBL; AP002541; BAB55470.1; -.
DR HSSP; P08631; 1AD5.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR004040; STY_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR SMART; SM00221; STYKc; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; P500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; P250011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Receptor; Transferase.
SQ SEQUENCE 636 AA; 70968 MW; E6805D9E1DF43462 CRC64;

Query Match 12.4%; Score 73; DB 10; Length 636;
Best Local Similarity 27.0%; Pred. No. 14;
Matches 24; Conservative 13; Mismatches 38; Indels 14; Gaps:

QY 12 KLCADCECVYTISLASQBDYNAPDC----RFNVKGGQIYVYKLVKENGAGEFWAGSV 683
Db 480 KLCARDQSIITLTAARGTMGTIAPELYSRNFEISYKSDVYFSGMLVL-----EMVSGRR 533

QY 69 YGDGQDEMGVGVFPRNLVKEQRYQEAT 97
Db 535 NSDPSPVESQNVVFP-----EWIYEQT 557

RESULT 15
ID Q9FU04 PRELIMINARY; PRT; 643 AA.
AC Q9FU04;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE RECEPTOR KINASE.
GN P0698G03.26 OR P0494A10.4.
OS Oryza sativa (Rice).

```

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone:P0698G03.;"

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. NIPPONBARE;

RA Sasaki T., Matsumoto T., Yamamoto K.;

RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

RT clone:P0494A10.;"

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF002747; BAB17342.1; -

DR EMBL; AP002541; BAB55464.1; -

DR HSSP; P08631; IADS.

DR InterPro: IPR000719; Euk_pkinase.

DR InterPro: IPR002290; Ser_thr_pkinase.

DR InterPro: IPR004040; STY_pkinase.

DR InterPro: IPR001245; Tyr_pkinase.

DR Pfam: PF00069; pkinase; 1.

DR SMART; SM00221; STYK; 1.

DR SMART; SM00220; S_TKG; 1.

DR SMART; SM00219; TYRK; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

KW ATP-binding; Kinase; Receptor; Transferase.

SQ SEQUENCE 643 AA; 71525 MW; BFB45CB172A6F15A CRC64;

Query Match

Best Local Similarity 12.4%; Score 73; DB 10; Length 643;

Matches 31; Conservative 15; Mismatches 52; Indels 22; Gaps 4;

QY 1 HGIFMDRLAS-----KKLCADDECVTYISLASAQEDYNAPDC---RFINVKKGQIY 49

Db 477 HNLLDYNFSPKISDFGLAKLCARDQSIVTLTAAGTGMGYIAPELYSRNFGSEISKSDVY 536

QY 50 VYSKLYKENGAGFEWAGSVYGDQDEMGVGYFPR-----NLVKEQRYVQEAATKEVPTT 103

Db 537 SFGMLVL-----EMVSGRRNSDPVSESONVYFPPEWYIEQVNSGODLALGREMTQEEKET 591

Search completed: September 23, 2002, 09:41:26

Job time: 246 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2002, 09:36:50 ; Search time 30.16 Seconds
(Without alignments)
405.110 Million cell updates/sec

Title: US-10-019-455A-24

Perfect score: 590

Sequence: 1 HGIFMDRLASKKLCADCEV.....RVYQATKEVPTTIDIDFCE 110

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_032802.*
- 1: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
 - 2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
 - 3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
 - 4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
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 - 9: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
 - 10: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
 - 11: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
 - 12: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
 - 13: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
 - 15: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
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 - 19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	590	100.0	110	22	Human MLP protein
2	590	100.0	128	22	Human growth regul
3	590	100.0	128	22	Human MLP protein
4	561	95.1	105	22	Human growth regul
5	547	92.7	110	22	Mouse MLP protein
6	547	92.7	128	22	Mouse MLP protein
7	541	91.7	110	22	Rat MLP protein se
8	541	91.7	128	22	Rat MLP protein se
9	417	70.7	87	22	Rat MLP protein se
10	253.5	43.0	131	16	Melanoma inhibiti
11	253.5	43.0	131	22	Human MIA protein

12	251.5	42.6	137	22	AAG65615	Recombinant human
13	231.5	39.2	130	15	AAR69812	Melanoma inhibiti
14	226.5	38.4	138	22	AAM25834	Human protein sequ
15	225.5	38.2	410	21	AAU70210	Human TANGO 130 pr
16	217	36.8	499	22	AAU29319	Human PRO polypept
17	215	36.4	303	22	AAU29304	Human PRO polypept
18	215	36.4	303	22	AAB87608	Human PRO19670. H
19	215	36.4	714	21	AAU70209	Murine TANGO 130 p
20	185.5	31.4	1369	20	AAU24788	Human secreted pro
21	185.5	31.4	1369	22	AAU39009	Human secreted pro
22	179.5	30.4	114	21	AAG03662	Human secreted pro
23	179.5	30.4	192	22	AAU14154	Human novel protei
24	167	28.3	90	22	AAU14390	Human novel protei
25	157.5	26.7	98	21	AAU84900	A human proliferat
26	100	16.9	21	22	AAB69128	Mouse MLP peptide
27	88.5	15.0	318	19	AAB69429	Human secreted pro
28	86.5	14.7	287	20	AAU22236	Human KDR signal t
29	86.5	14.7	797	20	AAU27125	Amino acid sequenc
30	86.5	14.7	845	21	AAU49419	PKA substrate, Vav
31	86.5	14.7	847	20	AAU22237	Human KDR signal t
32	85.5	14.5	844	13	AAR25671	Mouse vav proto on
33	82.5	14.0	498	22	AAB95643	Human protein sequ
34	79.5	13.5	186	22	ABU10242	Human CDNA SEQ ID
35	78.5	13.3	1589	21	ABU68822	Amino acid sequenc
36	72	12.2	462	17	AAW05395	Human SH3P17 prote
37	72	12.2	641	20	AAU32158	Human SH3D1A prote
38	72	12.2	1144	20	AAU32154	Human SH3D1A prote
39	71	12.0	2091	21	AAU12000	Rat p3103 protein.
40	70.5	11.9	663	19	AAB49872	Thermotoga maritim
41	70.5	11.9	680	18	AAW34564	Thermotoga maritim
42	70.5	11.9	680	19	AAW49868	Thermotoga maritim
43	70.5	11.9	680	19	AAW35005	Thermotoga maritim
44	70	11.9	280	19	AAW77273	Protease PD498 mut
45	70	11.9	1683	21	AAU71160	Rat phosphodiester

ALIGNMENTS

RESULT 1
AAB69126
ID AAB69126 standard; Protein; 110 AA.
AC AAB69126;
XX 23-APR-2001 (first entry)
DT Human MLP protein sequence SEQ ID NO:24.
DE
KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
cardiant; gene therapy; secretory cell function regulator; promoter;
inhibitor.
KW Homo sapiens.
OS
XX
XX WO200102564-A1.
PN
XX
PD 11-JAN-2001.
PF 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
Tanaka H;
XX
XX WPI; 2001-159271/16.
DR N-PSDB; AAF59079.
XX
XX Safe, low-toxicity secretory cell function-regulatory protein and

PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -

PS Claim 1; Page 97-98; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 110 AA;

Query Match 100.0%; Score 590; DB 22; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.1e-68;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENG 60

Db 1 hgifmdrlaskklcaddecvtyslasaqedynapdcrfinvkkgqiyvysklvkenga 60

Qy 61 GEFWAGSVYGDQDEMGVVGYPFPRNLVKQRVYQATKEVPTDIDFFCE 110

Db 61 gefwagsvygdqdemgvvgvfprnlvkeqrvyqeatkevpttdidffce 110

RESULT 2

AAB82671
ID AAB82671 standard; Protein; 128 AA.

AC AAB82671;

DT 02-OCT-2001 (first entry)

DE Human growth regulatory-like polypeptide.

KW Growth regulatory-like polypeptide; human; cartilage; melanoma;
KW neuroectodermal tumour; glioma; cancer; therapy; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= Signal_peptide

FT Protein 24..128

FT /label= Mature_protein

FT /note= "separately claimed in Claim 10"

FT WO200155332-A2.

PN 02-AUG-2001.

PD 25-JAN-2001; 2001WO-US02455.

PE 25-JAN-2000; 2000US-0491404.

PR 02-MAY-2000; 2000US-0563786.

XX (HYSE-) HYSEQ INC.

XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;

PI Drmanac RT;

XX WPI; 2001-483233/52.

DR N-PSDB; AAB26343;

XX Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders, and
PT hyperproliferative disorders, coagulation disorders, and nervous system

PT disorders -

PS Claim 10; Page 116-117; 119pp; English.

XX The present sequence is that of a novel human growth regulatory-like
CC polypeptide (GRLP). The amino acid sequence is predicted from a
CC novel assembled cDNA (see AAB26343) based on Hyseq clone number
CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polypeptides, which include the GRLP mature protein,
CC may also have nutritional uses, cytokine and cell proliferation,
CC or differentiation activity, stem cell growth factor activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC immunosuppressive or immunostimulant activity, activin/inhibin
CC activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, use in cancer diagnosis and therapy,
CC drug screening, receptor/ligand activity, antiinflammatory
CC activity, and treatment of leukaemia, nervous system disorders,
CC arthritis and inflammation.

XX Sequence 128 AA;

Query Match 100.0%; Score 590; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.4e-68;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGIFMDRLASKKLCADDECVTYISLASAQEDYNAPDCRFINVKKGQIYVYSKLVKENG 60

Db 19 hgifmdrlaskklcaddecvtyslasaqedynapdcrfinvkkgqiyvysklvkenga 78

Qy 61 GEFWAGSVYGDQDEMGVVGYPFPRNLVKQRVYQATKEVPTDIDFFCE 110

Db 79 gefwagsvygdqdemgvvgvfprnlvkeqrvyqeatkevpttdidffce 128

RESULT 3

AAB69123
ID AAB69123 standard; Protein; 128 AA.

AC AAB69123;

DT 23-APR-2001 (first entry)

DE Human MLP protein sequence SEQ ID NO:6.

XX MLP; MIA; melanoma inhibitory activity; cancer; bone disease;
KW joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
KW cardiant; gene therapy; secretory cell function regulator; promoter;
KW inhibitor.

OS Homo sapiens.

PN WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;
DR WPI: 2001-159271/16.
DR N-PSDB; AAF59065.
XX
PT Safe, low-toxicity secretory cell function-regulatory protein and
XX encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases
XX
XX Claim 2; Page 91-92; 111pp; Japanese.
XX
XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
XX in the exemplification of the present invention.
SQ Sequence 128 AA;

Query Match 100.0%; Score 590; DB 22; Length 128;
Best Local Similarity 100.0%; Pred. No. 1.4e-68;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVSKLVKNGA 60
DB 19 hglfmdrlaskklcaddecvtitslasagedynapdcrfinvkkgqgiyvsklvknga 78

QY 61 GEFWAGSVYGDQDEMVGVGYPFRNLVKEQRYQVQATKEVPTTDDIDFCE 110
DB 79 gefwagsvygdqdemvgvgypfrnlvkeqrvyqeatkevpttdidfice 128

RESULT 4
AAB82672
ID AAB82672 standard; Protein; 105 AA.
AC AAB82672;
XX
XX 02-OCT-2001 (first entry)
XX
DE Human growth regulatory-like polypeptide (mature protein).
Growth regulatory-like polypeptide; human; cartilage; melanoma;
neuroectodermal tumour; glioma; cancer; therapy; diagnosis.
XX
XX Homo sapiens.
XX
XX WO200155332-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US02455.
XX
XX 25-JAN-2000; 2000US-0491404.
XX
XX 02-MAY-2000; 2000US-0563786.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Mize NK, Boyle BJ, Ford JE, Arterburn MC, Tang YT, Liu C;
PI Drmanac RT;
XX
XX WPI: 2001-483233/52.
XX N-PSDB; AAB26343.
XX
XX Isolated human growth regulatory-like polypeptide useful for treating
PT e.g. Alzheimer's disease, cancer, autoimmune disorders,
PT hyperproliferative disorders, coagulation disorders, and nervous system

PT disorders -
XX
XX Claim 10; Page 117; 119pp; English.
XX
XX The present sequence is that of a novel human growth regulatory-like
CC polypeptide (GRLP) mature protein. The sequence is predicted from
CC a novel assembled cDNA (see AAB26343) based on Hyseq clone number
CC 16372272. The protein has a mol.wt. of 14 kDa unglycosylated. GRLP
CC belongs to the same protein family as growth regulatory proteins,
CC growth factors, human melanoma derived growth regulatory protein,
CC precursor (64% similarity and 45% identity over 111 amino acids)
CC or melanoma inhibitory activity, cattle cartilage-derived
CC retinoic acid sensitive protein (CD-RAP, 44% identity and 64%
CC similarity over 126 amino acids) and other retinoic acid-sensitive
CC proteins. GRLP polypeptides and polynucleotides of the invention
CC can be used in the prophylaxis, treatment (including gene therapy)
CC and diagnosis of disorders and diseases caused by, or involving,
CC cartilage development and maintenance, inhibition of melanoma cell
CC growth and tumours, including neuroectodermal tumours such as
CC gliomas. The polypeptides, which include the GRLP mature protein,
CC may also have nutritional uses, cytokine and cell proliferation
CC or differentiation activity, stem cell growth factor activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC immunosuppressive or immunostimulant activity, activin/inhibin
CC activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, use in cancer diagnosis and therapy,
CC drug screening, receptor/ligand activity, antiinflammatory
CC activity, and treatment of leukaemia, nervous system disorders,
CC arthritis and inflammation.
XX
XX Sequence 105 AA;

Query Match 95.1%; Score 561; DB 22; Length 105;
Best Local Similarity 100.0%; Pred. No. 6.2e-65;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 DRLASKKLCADDECVTITSLASAOEDYNAPDCRFINVKKGQOIYVSKLVKENGAEFFWA 65
DB 1 drlaskklcaddecvtitslasagedynapdcrfinvkkgqgiyvsklvkengaeffwa 60

QY 66 GSVYGDQDEMVGVGYPFRNLVKEQRYQVQATKEVPTTDDIDFCE 110
DB 61 gsvygdqdemvgvgypfrnlvkeqrvyqeatkevpttdidfice 105

RESULT 5
AAB69127
ID AAB69127 standard; Protein; 110 AA.
XX
XX AAB69127;
XX
XX 23-APR-2001 (first entry)
XX
XX Mouse MLP protein sequence SEQ ID NO:26.
XX
XX
XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.
XX
XX Mus musculus.
XX
XX WO200102564-A1.
XX
XX 11-JAN-2001.
XX
XX 29-JUN-2000; 2000WO-JP04278.
XX
XX 30-JUN-1999; 99JP-0186718.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;
XX
DR WPI: 2001-159271/16.
DR N-PSDB; AAF59080.
XX

PT Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX

XX Claim 3; Page 98-99; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 110 AA;

Query Match 92.7%; Score 547; DB 22; Length 110;
Best Local Similarity 90.0%; Pred. No. 4.4e-63;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMRLASKKLCADDECYVTISLASAQEDYNAPDCRFNVKKGQIYVYKLVKNGA 60
DB 1 hgvmfmdklsskklcadeecvvtislaragedynapdcridvkkqgiyvysklvtenga 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GEFWAGSVYGDGDEMGVYGFPRNLVKEQRYVQATKEVPTDIDFFCE 110
DB 61 gefwagsvygdhgqdegivgyfpsnlvkeqrvyqeatkeiptddidffce 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
AAB69125

ID AAB69125 standard; Protein; 128 AA.

XX AAB69125;

XX 23-APR-2001 (first entry)

XX Mouse MLP protein sequence SEQ ID NO:12.

XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.

XX Mus musculus.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;

XX WPI: 2001-159271/16.

XX N-PSDB; AAF59068.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of

PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX
PS Claim 4; Page 93-94; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 128 AA;

Query Match 92.7%; Score 547; DB 22; Length 128;
Best Local Similarity 90.0%; Pred. No. 5.4e-63;
Matches 99; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 HGFMRLASKKLCADDECYVTISLASAQEDYNAPDCRFNVKKGQIYVYKLVKNGA 60
DB 19 hgvmfmdklsskklcadeecvvtislaragedynapdcridvkkqgiyvysklvtenga 78
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GEFWAGSVYGDGDEMGVYGFPRNLVKEQRYVQATKEVPTDIDFFCE 110
DB 79 gefwagsvygdhgqdegivgyfpsnlvkeqrvyqeatkeiptddidffce 128
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 7
AAB69131

ID AAB69131 standard; Protein; 110 AA.

XX AAB69131;

XX 23-APR-2001 (first entry)

XX Rat MLP protein sequence SEQ ID NO:49.

XX MLP; MTA; melanoma inhibitory activity; cancer; bone disease;
XX joint disease; pathologic angiogenesis; diagnosis; antiinflammatory;
XX cardiant; gene therapy; secretory cell function regulator; promoter;
XX inhibitor.

XX Rattus sp.

XX WO200102564-A1.

XX 11-JAN-2001.

XX 29-JUN-2000; 2000WO-JP04278.

XX 30-JUN-1999; 99JP-0186718.

XX (TAKE) TAKEDA CHEM IND LTD.

XX Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
PI Tanaka H;

XX WPI: 2001-159271/16.

XX N-PSDB; AAF59099.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases -
XX

XX Claim 5; Page 107; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell

CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 110 AA;

Query Match 91.7%; Score 541; DB 22; Length 110;
Best Local Similarity 89.1%; Pred. No. 2.6e-62;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKRENGA 60

DB 1 hgmfdklsskklcadeecvytislaragedynapdcrcfinvkkqgiyysklvtenga 60

QY 61 GEFWAGSVYGDGDEMVGVPFRNLVKEQRYQATKEVPTTIDIFFCE 110

61 gairwagsvygdhqdmgivgyfnsnlvreqrvygeatkeipttdidffce 110

RESULT 8

AAB69130

ID AAB69130 standard; Protein; 128 AA.

XX AC AAB69130;

XX DT 23-APR-2001 (first entry)

XX DE Rat MLP protein sequence SEQ ID NO:47.

XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

XX KW joint disease; pathologic angiogenesis; diagnosis; antinflammatory;

XX KW cardiant; gene therapy; secretory cell function regulator; promoter;

XX KW inhibitor.

XX OS Rattus sp.

XX PN WO200102564-A1.

XX PD 11-JAN-2001.

XX PF 29-JUN-2000; 2000WO-JP04278.

XX PR 30-JUN-1999; 99JP-0186718.

XX PR (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;

DR WPI; 2001-159271/16.

DR N-PSDB; AAF59098.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases

XX PS Claim 6; Page 106; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 128 AA;

Query Match 91.7%; Score 541; DB 22; Length 128;
Best Local Similarity 89.1%; Pred. No. 3.3e-62;
Matches 98; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 HGIFMDRLASKKLCADDECYVTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKRENGA 60

DB 19 hgmfdklsskklcadeecvytislaragedynapdcrcfinvkkqgiyysklvtenga 78

QY 61 GEFWAGSVYGDGDEMVGVPFRNLVKEQRYQATKEVPTTIDIFFCE 110

61 gairwagsvygdhqdmgivgyfnsnlvreqrvygeatkeipttdidffce 128

RESULT 9

AAB69129

ID AAB69129 standard; Protein; 87 AA.

XX AC AAB69129;

XX DT 23-APR-2001 (first entry)

XX DE Rat MLP protein sequence SEQ ID NO:39.

XX KW MLP; MIA; melanoma inhibitory activity; cancer; bone disease;

XX KW joint disease; pathologic angiogenesis; diagnosis; antinflammatory;

XX KW cardiant; gene therapy; secretory cell function regulator; promoter;

XX KW inhibitor.

XX OS Rattus sp.

XX PN WO200102564-A1.

XX PD 11-JAN-2001.

XX PF 29-JUN-2000; 2000WO-JP04278.

XX PR 30-JUN-1999; 99JP-0186718.

XX PR (TAKE) TAKEDA CHEM IND LTD.

PI Itoh Y, Nishi K, Ogi K, Ohkubo S, Mogi S, Noguchi Y, Yoshimura K;
XX Tanaka H;

DR WPI; 2001-159271/16.

XX Safe, low-toxicity secretory cell function-regulatory protein and
PT encoded DNA, applicable as drugs, in diagnosis and development of
PT promoters and inhibitors for preventing or treating e.g. bone and joint
PT diseases

XX PS Example 9; Page 103; 111pp; Japanese.

XX The present invention describes novel MLP proteins and their encoding
CC DNAs. The MLP proteins and DNAs have antiinflammatory and cardiant
CC activities, and can be used in gene therapy and as secretory cell
CC function regulators. The MLP proteins and DNAs can be used in drugs, in
CC the diagnosis and development of promoters and inhibitors for preventing
CC or treating bone and joint diseases as well as pathologic angiogenesis.
CC AAF59063 to AAF59099 and AAB69122 to AAB69132 represent sequences used
CC in the exemplification of the present invention.

XX Sequence 87 AA;

Query Match 70.7%; Score 417; DB 22; Length 87;
Best Local Similarity 88.5%; Pred. No. 2.6e-46;
Matches 77; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 6 DRLASKKLCADDECYVTISLASAQEDYNAPDCRFINVKKGQOIYVYSKLVKRENGA 65

DB 1 dklskklcadeecvytislaragedynapdcrcfinvkkqgiyysklvtengagafwa 60

QY 66 GSVYGDQDEMGVGVYFPNRLVKEQRY 92
 Db 61 gsvygdhqdgmigvgyfpsnlvreqrv 87

RESULT 10

AAR69811
 ID AAR69811 standard; Protein; 131 AA.

XX AAR69811;
 AC AAR69811;

DT 26-OCT-1995 (first entry)
 XX

DE Melanoma inhibiting protein (human).
 XX

XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;
 KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;
 KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
 KW probe; fusion protein.
 XX

XX Homo sapiens.
 S

XX WO9503328-A.
 N

XX 02-FEB-1995.
 PD

XX 19-JUL-1994; 94WO-EP02369.
 PF

XX 20-JUL-1993; 93DE-4324247.
 PR

XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 PA

XX Bogdahn U, Buettner R, Kaluza B;
 PI

XX WPI: 1995-075191/10.
 DR

XX N-PSDB; AAQ84050, AAQ84051.
 DR

XX New melanoma inhibiting protein and related nucleic acid -
 CC

PT vectors, transformed cells, antibodies etc., useful for treating
 PT tumours and as immunosuppressant e.g. by gene therapy

XX Claim 1; Page 54; 85pp; German.
 PS

XX This protein has melanoma-inhibiting activity and can be used to
 CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
 CC lung cancer, neuroectodermal tumours) or as an immunosuppressant
 CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
 CC peripheral blood lymphocytes). Antibodies raised against the
 CC protein can be used to detect cell producing the protein and also
 CC for protein purification. Probes derived from DNA encoding the
 CC protein (AAQ84050, AAQ84051) can be used to detect sequences encoding
 CC the protein or related proteins. The protein may be expressed as
 CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).
 XX

SQ Sequence 131 AA;

Query Match 43.0%; Score 253.5; DB 16; Length 131;
 Best Local Similarity 45.4%; Pred. No. 8.7e-25;
 Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADDECYVTTISLASAEDYNAPDCRFINVKKGQOIYVYSLVKVENGAGE-F 63

Db 27 mpkladrklcadqecshpismavalqdympdcrcfithrgqvvyvfskl---kgrgrlf 83

QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKEQRYQEQATKEVPTTDDIFCE 110

Db 84 wggsvggdygylaarlgvfpsslvredqtlkpgkvdvtdkwdlycq 131

RESULT 11

AAG65614
 ID AAG65614 standard; Protein; 131 AA.

XX

AC AAG65614;

DT 07-JAN-2002 (first entry)

DE Human MIA protein sequence.

XX MIA; melanoma inhibiting activity protein; antiinflammatory; human;
 KW antiarthritic; antirheumatic; antithyroid; osteopathic; nephrotropic;
 KW immunosuppressive; ophthalmological; dermatological; antidiabetic;
 KW neuroprotective; immune tolerance; T-cell tolerance.

OS Homo sapiens.

XX WO200170253-A1.

XX 27-SEP-2001.

PD 15-MAR-2001; 2001WO-EP02991.

PF 23-MAR-2000; 2000EP-0201063.

XX (ALKU) AKZO NOBEL NV.

PA Nelissen RLH, Verheijden GFM;

PI WPI: 2001-611446/70.

XX N-PSDB; AAH47783.

XX Use of melanoma inhibiting activity protein or its derivatives as
 PT immune modulatory agents for the treatment of inflammatory diseases,
 PT specifically rheumatoid arthritis -

XX Example 4; Page 34; 41pp; English.

XX The invention relates to the use of melanoma inhibiting activity (MIA)
 CC protein and/or its fragments that have anti-inflammatory effects and
 CC induce systemic immune tolerance or specific T-cell tolerance to MIA
 CC antigen, for manufacturing a preparation against inflammatory diseases
 CC and for induction of systemic immune tolerance or specific T-cell
 CC tolerance in patients suffering from or susceptible to inflammatory
 CC diseases. A fragment of MIA is useful as a therapeutic substance and is
 CC useful for manufacture of pharmaceutical preparations against
 CC inflammatory diseases such as an immune-cell mediated cartilage
 CC destruction disease, specifically rheumatoid arthritis, autoimmune
 CC diseases like Graves' disease, juvenile arthritis, primary
 CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,
 CC myasthenia gravis, Addison's disease, primary biliary sclerosis,
 CC uveitis, systemic lupus erythematosus, inflammatory bowel disease,
 CC multiple sclerosis or diabetes. The MIA polypeptides have specific
 CC effect on the autoreactive T-cells thus leaving the other components of
 CC the immune system intact as compared to the non-specific suppressive
 CC effect of immunosuppressive drugs. The present sequence represents a
 CC human MIA protein.

XX Sequence 131 AA;

Query Match 43.0%; Score 253.5; DB 22; Length 131;
 Best Local Similarity 45.4%; Pred. No. 8.7e-25;
 Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADDECYVTTISLASAEDYNAPDCRFINVKKGQOIYVYSLVKVENGAGE-F 63

Db 27 mpkladrklcadqecshpismavalqdympdcrcfithrgqvvyvfskl---kgrgrlf 83

QY 64 WAGSVYGDQDEMGV-VGYFPRNLVKEQRYQEQATKEVPTTDDIFCE 110

Db 84 wggsvggdygylaarlgvfpsslvredqtlkpgkvdvtdkwdlycq 131

RESULT 12

AAG65615

ID AAG5615 standard; Protein; 137 AA.

XX AC AAG5615;

XX DT 07-JAN-2002 (first entry)

XX DE Recombinant human MIA(his7) protein.

XX MIA; melanoma inhibiting activity protein; antiinflammatory; human;
KW antirheumatic; antirheumatic; antithyroid; osteopathic; nephrotropic;
KW immunosuppressive; ophthalmological; dermatological; antidiabetic;
KW neuroprotective; immune tolerance; T-cell.

XX OS Homo sapiens.

XX PN WO200170253-A1.

XX PD 27-SEP-2001.

XX 15-MAR-2001; 2001WO-EP02991.

XX 23-MAR-2000; 2000EP-0201063.

XX (ALKU) AKZO NOBEL NV.

XX PA Nelissen RLH, Verheijden GFM;

XX PI WPI; 2001-611446/70.

XX DR N-PSDB; AAH47783.

XX Use of melanoma inhibiting activity protein or its derivatives as
PT immune modulatory agents for the treatment of inflammatory diseases,
PT specifically rheumatoid arthritis -

XX Example 1; Page 35; 41pp; English.

XX The invention relates to the use of melanoma inhibiting activity (MIA)
CC protein and/or its fragments that have anti-inflammatory effects and
CC induce systemic immune tolerance or specific T-cell tolerance to MIA
CC antigen, for manufacturing a preparation against inflammatory diseases
CC and for induction of systemic immune tolerance or specific T-cell
CC tolerance in patients suffering from or susceptible to inflammatory
CC diseases. A fragment of MIA is useful as a therapeutic substance and is
CC useful for manufacture of pharmaceutical preparations against
CC inflammatory diseases such as an immune-cell mediated cartilage
CC destruction disease, specifically rheumatoid arthritis, autoimmune
CC diseases like Graves' disease, juvenile arthritis, primary
CC glomerulonephritis, polyarthritis, osteoarthritis, Sjogren's syndrome,
CC myasthenia gravis, Addison's disease, primary biliary sclerosis,
CC uveitis, systemic lupus erythematosus, inflammatory bowel disease,
CC multiple sclerosis or diabetes. The MIA polypeptides have specific
CC effect on the autoreactive T-cells thus leaving the other components of
CC the immune system intact as compared to the non-specific suppressive
CC effect of immunosuppressive drugs. The present sequence represents a
CC cDNA encoding a human recombinant MIA(his7) protein.

XX Sequence 137 AA;

Query Match 42.6%; Score 251.5; DB 22; Length 137;
Best Local Similarity 45.8%; Pred. No. 1.7e-24;
Matches 49; Conservative 20; Mismatches 33; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADCECVYTISLASAQEDYNAPDCRFNVKKGQIYVYVKLVKENGAGE-F 63

Db 27 mpkladrkicadeqchspismavalqdynapdcrcfritihrgvqvvyfskl---kgrgrlf 83

QY 64 WAGSVYGDGDQDEMGV-VGYFPPRLNVKEQRYQVQATKEVPTDIDFFC 109

Db 84 wgsgvgygdygdlaarlgypfssivredgtlpgkdvtkdkwdfyc 130

RESULT 13

AAR69812

ID AAR69812 standard; Protein; 130 AA.

XX AC AAR69812;

XX DT 26-OCT-1995 (first entry)

XX DE Melanoma inhibiting protein (murine).

XX Melanoma; inhibition; cancer; melanoma; glioblastoma; neuroblastoma;
KW small cell lung cancer; neuroectodermal tumours; immunosuppressant;
KW phytohaemagglutinin; lymphocyte; interleukin 2; IL-2; detection;
KW probe; fusion protein.

XX OS Mus musculus.

XX PN WO9503328-A.

XX PD 02-FEB-1995.

XX 19-JUL-1994; 94WO-EP02369.

XX 20-JUL-1993; 93DE-4324247.

XX (BOEF) BOEHRINGER MANNHEIM GMBH.

XX Bogdahn U, Buettner R, Kaluza B;

XX WPI; 1995-075191/10.

XX N-PSDB; AAQ45052.

XX New melanoma inhibiting protein and related nucleic acid -
PT vectors, transformed cells, antibodies etc., useful for treating
PT tumours and as immunosuppressant e.g. by gene therapy

XX Claim 5; Page 60; 85pp; German.

XX This protein has melanoma-inhibiting activity and can be used to
CC treat cancer (melanoma, glioblastoma, neuroblastoma, small cell
CC lung cancer, neuroectodermal tumours) or as an immunosuppressant
CC (it inhibits IL-2 or phytohaemagglutinin induced proliferation of
CC peripheral blood lymphocytes). Antibodies raised against the
CC protein can be used to detect cell producing the protein and also
CC for protein purification. Probes derived from DNA encoding the
CC protein (AAQ84052) can be used to detect sequences encoding the
CC protein or related proteins. The protein may be expressed as
CC a fusion protein (conjugated with dihydrofolate reductase (DHFR)).

XX Sequence 130 AA;

Query Match 39.2%; Score 231.5; DB 16; Length 130;
Best Local Similarity 43.5%; Pred. No. 6.3e-22;
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADCECVYTISLASAQEDYNAPDCRFNVKKGQIYVYVKLVKENGAGE-F 63

Db 26 mpkladrkicadeqchspismavalqdynapdcrcfritihrgvqvvyfskl---kgrgrlf 82

QY 64 WAGSVYGDGDQDEMGV-VGYFPPRLNVKEQRYQVQATKEVPTDIDFFC 110

Db 83 wgsgvgygdygdlaarlgypfssivredgtlpgkdvtkdkwdfyc 130

RESULT 14

AAM25834

ID AAM25834 standard; Protein; 138 AA.

XX AC AAM25834;

XX DT 16-OCT-2001 (first entry)

XX Human protein sequence SEQ ID NO:1349.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
KW antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
KW antibacterial; endocrine; cardiant; central nervous system; virucide;
KW anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
KW antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema;
KW dermatological; anti-allergic; antiasthmatic; antidiabetic; cytostatic;
KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;
KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.
XX Homo sapiens.
XX OS
XX WO200153455-A2.
XX 26-JUL-2001.
XX 22-DEC-2000; 2000WO-US35017.
XX 23-DEC-1999; 99US-0471275.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457603/49.
XX N-PSDB; AAH99775.
XX Isolated human polynucleotides encoding polypeptides, useful for the
XX treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX Claim 20; Page 279; 1217pp; English.
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
XX AAM25963. The proteins can have activities based on the tissues and
XX cells they are expressed in, such as: antiinflammatory; antirheumatic;
XX antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
XX central nervous system; virucide; anti-HIV; fungicide; antimutagen;
XX cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary;
XX antiulcer; osteopathic; dermatological; anti-allergic; antiasthmatic;
XX antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
XX antiparkinsonian; and immunostimulant. The proteins and polynucleotides
XX encoding them can be used in gene therapy, antisense therapy and vaccine
XX production. The proteins and polynucleotides are useful for screening for
XX agonists or antagonists of a protein and for the treatment and diagnosis
XX of disorders associated with the activity of a protein e.g. inflammation,
XX rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
XX neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
XX infections, autoimmunity, genetic diseases, haematopoietic disorders,
XX anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
XX osteoporosis, severe combined immunodeficiency, eczema, allergic
XX rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
XX Alzheimer's disease, Parkinson's disease, neurodegenerative and
XX neurological disorders.
XX Sequence 138 AA;

Query Match 38.4%; Score 226.5; DB 22; Length 138;
Best Local Similarity 44.7%; Pred. No. 3.1e-21;
Matches 46; Conservative 14; Mismatches 34; Indels 9; Gaps 3;
QY 7 RLASKKLCADCCSLMYRGEALDFTGDCRFVNFKXGDPVYVYKIA--GWPEVWAG 66
DB 32 RLSEKHLCAADCCSLMYRGEALDFTGDCRFVNFKXGDPVYVYKIA--GWPEVWAG 89

QY 67 SVYGDQDGMGVGYEPNVLVKQRVYQVQATKEVPTTIDDFC 109
DB 90 sv---gr----tfgyfkdliqvvhvhtkeelqvptnetdfvc 125
RESULT 15
AAAY70210
ID AAAY70210 standard; Protein; 410 AA.
XX AAAY70210;
AC AAAY70210;
XX 06-JUN-2000 (first entry)
DT Human TANGO 130 protein.
DE
XX TANGO 130; human; hTANGO130; Melanoma-inhibiting protein; MIA; marker;
KW chromosome 4p1; chromosome 7; chromosome 14q; chromosome 18p1; tumour;
KW cytostatic; immunomodulatory; cell proliferation/differentiation;
KW chondrosarcoma; sarcoma; melanoma; diagnosis; epithelium; mesenchyma;
KW carcinoma; glioblastoma; modulator; cell-cell interaction; metastasis;
KW cell migration; retinoic acid; AP2 transcription factor; morphogenesis;
KW embryonic cell growth.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
FH Peptide 1..23
FT /label= Signal_peptide
FT Protein 24..410
FT /label= Mature_human_TANGO_130_protein
FT /note= "This region is specifically claimed"
FT Domain 1..125
FT /label= MIA_homology_domain
FT /note= "Homologous by 38% to human MIA"
XX
XX WO200012762-A1.
XX 09-MAR-2000.
XX 01-SEP-1999; 99WO-US20032.
XX 01-SEP-1998; 98US-0145056.
XX (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
XX Pan Y;
XX WPI; 2000-237889/20.
XX N-PSDB; AAZ51245.
XX Nucleic acids encoding human and murine TANGO 130, a
XX melanoma-inhibiting protein homolog, useful for modulating cell
XX proliferation and differentiation -
XX Claim 9; Fig 3; 128pp; English.
XX The present amino acid sequence is the human TANGO 130 protein
XX (hTANGO130). The gene is mapped to chromosomes 4p1, 7, 14q and 18p1.
XX Human TANGO 130 has highest expression in testis and also in heart,
XX brain, placenta, liver, lung, skeletal muscle, pancreas, kidney, spleen,
XX thymus, prostate and uterus. It has cytostatic and immunomodulatory
XX activity. TANGO 130, a homologue of melanoma-inhibiting protein (MIA),
XX inhibits growth of melanocytes and may be used to treat malignant
XX melanomas, chondrosarcomas and metastatic tumours. They serve as serum
XX markers for diagnosis and monitoring disease states. TANGO 130 inhibits
XX abnormal or malignant proliferation of cells of the heart, liver, testis,
XX kidney, immune system, CNS, skeleton, epithelial cells (e.g. carcinomas
XX and melanomas), mesenchymal cells (e.g. sarcomas, chondrosarcomas and
XX glioblastomas). It modulates cell-cell interactions (e.g. cell adhesion
XX or cell-substrate interactions), cell migration (e.g. abnormal migration
XX and metastasis of tumour cells), cell differentiation, retinoic acid-
XX mediated functions/activities, like modulation of AP2 transcription

CC factor function and embryonic cell growth/morphogenesis.

AA	Sequence	410 AA;
SQ		

Query Match	38.2%	Score 225.5;	DB 21;	Length 410;
Best Local Similarity	44.7%;	Pred. No. 1.9e-20;		
Matches 46:	Conservative	14;	Mismatches 34;	Indels 9; Gaps 3;

QY 7 RLASKKLCADDECYTTISLASAQEDYNAPDORFFINVKKGQQIYVYSKLVKENGAGEFWAG 66

Db 31 rfsehk lcaddecsm lmyrgealedftpcdrfynfkqdpvvyvyyklar--gwpevwaq 88

Qy 67 SVYGDQDEMVGVFPPRNLVKEQRVYQEATKEVPTTIDIDFFC 109

Db 89 sv---gr---tfqyfpkdlqvvvheytkeelqvptdetsfvc 124

Search completed: September 23, 2002, 09:37:53
 Elapsed time: 63 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2002, 09:36:50 ; Search time 12.89 Seconds
(without alignments)
208.442 Million cell updates/sec

Title: US-10-019-455A-24
Perfect score: 590
Sequence: 1 HGFMRLASKKLCADCECV.....RVQVETKVEPTTIDIFCEE 110

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Cal number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/PTCUTS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	253.5	43.0	131	1 US-08-578-649-2	Sequence 2, Appli
2	231.5	39.2	130	1 US-08-578-649-5	Sequence 5, Appli
3	85.5	14.5	844	1 US-07-646-537B-2	Sequence 2, Appli
4	81.5	13.8	54	4 US-09-346-510B-21	Sequence 21, Appli
5	78.5	13.3	1589	3 US-09-356-952-4	Sequence 4, Appli
6	72.5	12.3	48	4 US-09-346-510B-24	Sequence 24, Appli
7	72	12.2	462	4 US-08-630-915A-38	Sequence 38, Appli
8	66.5	11.3	62	4 US-08-630-915A-135	Sequence 135, Appli
9	66.5	11.3	642	2 US-08-245-511-48	Sequence 48, Appli
10	66.5	11.3	642	2 US-08-600-993A-48	Sequence 48, Appli
11	66	11.2	248	4 US-08-630-915A-40	Sequence 40, Appli
12	66	11.2	280	1 US-08-434-255-8	Sequence 8, Appli
13	66	11.2	280	1 US-08-459-967-8	Sequence 8, Appli
14	66	11.2	280	1 US-08-460-327-8	Sequence 8, Appli
15	66	11.2	280	1 US-08-459-871-8	Sequence 8, Appli
16	66	11.2	280	4 US-09-024-532-2	Sequence 2, Appli
17	66	11.2	280	4 US-09-104-623A-2	Sequence 2, Appli
18	66	11.2	370	1 US-08-434-255-6	Sequence 6, Appli
19	66	11.2	370	1 US-08-459-967-6	Sequence 6, Appli
20	66	11.2	370	1 US-08-460-327-6	Sequence 6, Appli
21	66	11.2	370	1 US-08-459-871-6	Sequence 6, Appli
22	66	11.2	397	1 US-08-434-255-2	Sequence 2, Appli
23	66	11.2	397	1 US-08-434-255-4	Sequence 4, Appli
24	66	11.2	397	1 US-08-459-967-2	Sequence 2, Appli
25	66	11.2	397	1 US-08-459-967-4	Sequence 4, Appli
26	66	11.2	397	1 US-08-460-327-2	Sequence 2, Appli
27	66	11.2	397	1 US-08-460-327-4	Sequence 4, Appli

28	66	11.2	397	1 US-08-459-871-2	Sequence 2, Appli
29	66	11.2	397	1 US-08-459-871-4	Sequence 4, Appli
30	66	11.2	509	4 US-08-630-915A-194	Sequence 194, App
31	65	11.0	57	4 US-08-630-915A-136	Sequence 136, App
32	64	10.8	57	4 US-08-630-915A-219	Sequence 219, App
33	64	10.8	433	1 US-08-700-359-20	Sequence 20, Appl
34	64	10.8	532	3 US-08-911-321-11	Sequence 11, Appl
35	64	10.8	803	1 US-08-158-232-10	Sequence 10, Appl
36	64	10.8	803	1 US-08-304-626-10	Sequence 10, Appl
37	64	10.8	803	1 US-08-316-301A-12	Sequence 12, Appl
38	64	10.8	803	2 US-08-611-928-10	Sequence 10, Appl
39	64	10.8	803	3 US-09-173-891-10	Sequence 10, Appl
40	64	10.8	803	4 US-09-076-137-12	Sequence 12, Appl
41	64	10.8	803	5 PCT-US92-03624-12	Sequence 12, Appl
42	63.5	10.8	58	4 US-08-630-915A-210	Sequence 210, App
43	63	10.7	57	4 US-08-630-915A-125	Sequence 125, App
44	63	10.7	543	4 US-08-426-509A-14	Sequence 14, Appl
45	63	10.7	543	5 PCT-US95-05008-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-578-649-2
; Sequence 2, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Buttner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajolloff
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 868-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-578-649-2

Query Match 43.0%; Score 253.5; DB 1; Length 131;
Best Local Similarity 45.4%; Pred. No. 1.9e-25;
Matches 49; Conservative 21; Mismatches 33; Indels 5; Gaps 3;
QY 5 MDRLASKKLCADCECVTTISLSAQEDINAPDCRFNVKKGQIYVYVKLVKENGAGE-F 63

Db 27 MPKLADKLCADQECSPHPSMAVALQDYNAPDCRFLTIHRGQVYVFSKL---KGRGLF 83
QY 64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQATKEVPTTDDIFPCE 110
Db 84 WGSVQGGYDGLAARLGIFPSSIVREDQTLKPGKVDVTKDWDFVCQ 131

RESULT 2

US-08-578-649-5
; Sequence 5, Application US/08578649
; Patent No. 5770366
; GENERAL INFORMATION:
; APPLICANT: Ulrich Bogdan
; APPLICANT: Reinhard Butner
; APPLICANT: Brigitte Kaluza
; TITLE OF INVENTION: MELANOMA-INHIBITING PROTEIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch 1.44 Mb storage diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/578,649
; FILING DATE: 29-July-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P.43 24 247.2
; FILING DATE: 20-July-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Andrew L. Tiajoloif
; REGISTRATION NUMBER: 31,575
; REFERENCE/DOCKET NUMBER: BOER 1035-PFF/ALT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 130 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;-08-578-649-5

Query Match 39.2%; Score 231.5; DB 1; Length 130;
Best Local Similarity 43.5%; Pred. No. 1.4e-22;
Matches 47; Conservative 21; Mismatches 35; Indels 5; Gaps 3;

QY 5 MDRLASKKLCADCECVYTISLASAEDYNAPDCRFLTNVKKGOIYVYSLVKVKGAGE-F 63
Db 26 MPKLADKLCADQECSPHPSMAVALQDYNAPDCRFLTIHRGQVYVFSKL---KGRGLF 82
QY 64 WAGSVYGDGQDEMGV-VGYFPRNLVKEQRVYQATKEVPTTDDIFPCE 110
Db 83 WGSVQGGYDGLAARLGIFPSSIVREDLNSKPGKIDMKTDQWDFVCQ 130

RESULT 3

US-07-646-537B-2
; Sequence 2, Application US/07646537B
; Patent No. 5348864
; GENERAL INFORMATION:
; APPLICANT: Barbacid, Mariano
; TITLE OF INVENTION: Vav Proto-Oncogene Protein

; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/646.537B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DG10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 921-5901
; TELEFAX: (609) 921-4526
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 844 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-646-537B-2

Query Match 14.5%; Score 85.5; DB 1; Length 844;
Best Local Similarity 31.4%; Pred. No. 0.021; 21; Indels 13; Gaps 3;
Matches 22; Conservative 14; Mismatches 14;

QY 26 ASAEQDYNAPDCRFLTNVKKGOIYVYSLVKVKGAGEFWAGSVYGDGQDEMGVYVFPFN 85
Db 786 AKARYDFCARDRSELKRGDII---KILNKKGGQGGWWRGEIYGR-----IGWFPSN 834
QY 86 LVKEQRVYQ 95
Db 835 YVEED--YSE 842

RESULT 4

US-09-346-510B-21
; Sequence 21, Application US/09346510B
; Patent No. 6281014
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; APPLICANT: Wang, Yinxiaung
; TITLE OF INVENTION: SH3-Containing Protein, DNA and Uses Thereof
; FILE REFERENCE: D6221CIP
; CURRENT APPLICATION NUMBER: US/09/346.510B
; CURRENT FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 08/871,732
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 21
; LENGTH: 54
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; NAME/KEY: Domain
; OTHER INFORMATION: amino acid sequence of Vav SH3 domain
US-09-346-510B-21

Query Match 13.8%; Score 81.5; DB 4; Length 54;
Best Local Similarity 32.3%; Pred. No. 0.0015;
Matches 20; Conservative 13; Mismatches 18; Indels 11; Gaps 2;

US-08-630-915A-135
; Sequence 135, Application US/08630915A
; Patent No. 6309820

GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.
; APPLICANT: HOFFMAN, No. 6309820h
; APPLICANT: KAY, Brian K.
; APPLICANT: FOWLKES, Dana M.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; TITLE OF INVENTION: USING SAME

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Misrock, S. Leslie

; REGISTRATION NUMBER: 18,972

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 135:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 62 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: peptide

US-08-630-915A-135

Query Match 11.3%; Score 66.5; DB 4; Length 62;

Best Local Similarity 26.6%; Pred. No. 0.17; Mismatches 29; Indels 7; Gaps 2;

Matches 17; Conservative 11; Mismatches 29; Indels 7; Gaps 2;

QY 25 LASAQEDYNAPDCRFINVKKGQIYYVSKLVKENGAEFGWAGSVYGDQDGMGVVGYFPR 84

Db 4 IAQVIASVTATGPEQLTLAPQLI-----LIRKNPGWGWEGELQARGKKRQ--IGWFFA 56

QY 85 NLVK 88

Db 57 NYVK 60

RESULT 9

US-08-245-511-48

; Sequence 48, Application US/08245511

; Patent No. 5928900

; GENERAL INFORMATION:

; APPLICANT: Masure, H Robert

; APPLICANT: Pearce, Barbara J

; APPLICANT: Tuomanen, Elaine

; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND

; TITLE OF INVENTION: CELLULAR VACCINES BASED THEREON

; NUMBER OF SEQUENCES: 58

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/245,511

FILING DATE: 18-MAY-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/116,541

FILING DATE: 01-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-069 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 48:

SEQUENCE CHARACTERISTICS:

LENGTH: 642 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Streptococcus pneumoniae

IMMEDIATE SOURCE:

CLONE: amia

FEATURE:

OTHER INFORMATION: NOTE: the reference contains a

OTHER INFORMATION: sequence error; the correct sequence shown below is obtain

OTHER INFORMATION: from GENBANK

PUBLICATION INFORMATION:

AUTHORS: Aloiing, et al.

JOURNAL: Mol. Microbiol.

VOLUME: 4

PAGES: 633-644

DATE: 1990

US-08-245-511-48

Query Match 11.3%; Score 66.5; DB 2; Length 642;

Best Local Similarity 22.5%; Pred. No. 4.4;

Matches 27; Conservative 20; Mismatches 44; Indels 29; Gaps 4;

QY 6 DRLASKKLCADCECVTISLASAQEDYNAPDCRFINVKKGQIYYVSKLVKEN-----58

Db 309 EKVATKKALLNDFRQALNFALDRSAYSQA-----INGKDAALAVRNLFVKPDFVSAGEK 364

QY 59 -----GAGFEWAGSVYGDQDGMGVVGYPRNLVKQRYVQEATKEVPTTIDIF 107

Db 365 TFGDLVAAQLPAYGDEWKGKVNLAGDQD-----GLF--NADKAKAEFRKAKKALEADGVQF 417

RESULT 10

US-08-600-993A-48

; Sequence 48, Application US/08600993A

; Patent No. 5981229

; GENERAL INFORMATION:

; APPLICANT: Masure, H Robert

; APPLICANT: Pearce, Barbara J

; APPLICANT: Tuomanen, Elaine

; TITLE OF INVENTION: BACTERIAL EXPORTED PROTEINS AND

; TITLE OF INVENTION: CELLULAR VACCINES BASED THEREON

NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,993A
FILING DATE: 1-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/245,511
FILING DATE: 18-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/116,541
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-069 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 642 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORGANISM: Streptococcus pneumoniae
IMMEDIATE SOURCE:
CLONE: amia
FEATURE:
OTHER INFORMATION: the reference contains a sequence error; the
OTHER INFORMATION: correct sequence shown below is obtained from GENBANK
PUBLICATION INFORMATION:
AUTHORS: Allosing, et al.
JOURNAL: Mol. Microbiol.
VOLUME: 4
PAGES: 633-644
DATE: 1990
US-08-600-993A-48

Query Match 11.3%; Score 66.5; DB 2; Length 642;
Best Local Similarity 22.5%; Pred. No. 4.4;
Matches 27; Conservative 20; Mismatches 44; Indels 29; Gaps 4;
QY 6 DRLASKKLCADCECVTISLASAQEDYNAPDCRFINVKKGQIYVYVSKLVKEN-----58
Db 309 EKVAITKALLNKDFRALFALDRSAYSQA-----INGKDGAAALAVRNLFVKPDFVSAGEK 364
QY 59 -----GAGEFWAGSVYGDGDMGVGYFFRNLYKEQRYOEATKEVPTTIDIF 107
Db 365 TFGDLVAQLPAVGDEWKGVNLADGQD-----GLF--NADKAEKPKAKALEADGVQF 417
RESULT 11
US-08-630-915A-40
; Sequence 40, Application US/08630915A
; Patent No. 6309820

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
ADDRESSEE: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: McCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,972
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-40
Query Match 11.2%; Score 66; DB 4; Length 248;
Best Local Similarity 30.4%; Pred. No. 1.4;
Matches 24; Conservative 7; Mismatches 24; Indels 24; Gaps 3;
QY 28 AQEDYNAPDCRFINVKKGQIYVYVSKLVKENGAGEFWAGSVYGDGDMGVGYFFRNLY 87
Db 190 AMYDYAANNEDELSEFSKGQLINYNK-----DDPDWQGEI-----NGVTGLFSPSNV 237
QY 88 KEORVYOEATKEVPTTIDID 106
Db 238 K-----MTTDS 244
RESULT 12
US-08-434-255-8
; Sequence 8, Application US/08434255
; Patent No. 5621089
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dambmann, Claus
; APPLICANT: Aaslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5621089o No. 5621089th disk of No. 5621089th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York

; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-434-255-8

Query Match 11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 29.6%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 22 TISLASAEDYNAPDCRFNVKKGQIYYVSKLVKENGAGFEWAGSVYGDGQDEMGVGY 81
|::: : ||| || : | : | | | | : | | | : | | |
Db 34 TVAVLDSGVYDYNHPDLARKVKGIDYDFIDRNNPMDLNGHGHVAGTVAADTNGIGVAGM 93
QY 82 FPRNLVKEQRV 92
| : : | |
Db 94 APDTKILAVRV 104

RESULT 13
US-08-459-967-8
; Sequence 8, Application US/08459967
; Patent No. 5622841
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dambmann, Claus
; APPLICANT: Aslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5622841o No. 5622841disk of No. 5622841th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,967
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-967-8

Query Match 11.2%; Score 66; DB 1; Length 280;

; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-967-8

Query Match 11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 29.6%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 22 TISLASAEDYNAPDCRFNVKKGQIYYVSKLVKENGAGFEWAGSVYGDGQDEMGVGY 81
|::: : ||| || : | : | | | | : | | | : | | |
Db 34 TVAVLDSGVYDYNHPDLARKVKGIDYDFIDRNNPMDLNGHGHVAGTVAADTNGIGVAGM 93
QY 82 FPRNLVKEQRV 92
| : : | |
Db 94 APDTKILAVRV 104

RESULT 14

US-08-460-327-8
; Sequence 8, Application US/08460327
; Patent No. 5622850
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dambmann, Claus
; APPLICANT: Aslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5622850o No. 5622850disk of No. 5622850th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,327
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agris Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-460-327-8

Query Match

Job time: 82 sec

Best Local Similarity 29.6%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 22 TISLASAQEDYNAPDGRFINVKKGQIYVYKLVKENGAGEFWAGSVYGGODEMGVVG 81
Db 34 TVAVLDGVDYVNHPLARKVIRGYDFIDRNNPMDLNGHGHVAGTVAADTNNIGVAGM 93
QY 82 FPNLVKEQRV 92
Db 94 APDTKILAVRV 104

RESULT 15

US-08-459-871-8
; Sequence 8, Application US/08459871
; Patent No. 5650326
; GENERAL INFORMATION:
; APPLICANT: Sloma, Alan P.
; APPLICANT: Outtrup, Helle
; APPLICANT: Dambmann, Claus
; APPLICANT: Aslyng, Dorrit
; TITLE OF INVENTION: ALKALINE PROTEASE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 56503260 No. 5650326disk of No. 5650326th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,871
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/434,255
; FILING DATE: 03-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Agis Dr., Cheryl H.
; REGISTRATION NUMBER: 34,086
; REFERENCE/DOCKET NUMBER: 3764.400-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-459-871-8

Query Match 11.2%; Score 66; DB 1; Length 280;
Best Local Similarity 29.6%; Pred. No. 1.6;
Matches 21; Conservative 11; Mismatches 39; Indels 0; Gaps 0;

QY 22 TISLASAQEDYNAPDGRFINVKKGQIYVYKLVKENGAGEFWAGSVYGGODEMGVVG 81
Db 34 TVAVLDGVDYVNHPLARKVIRGYDFIDRNNPMDLNGHGHVAGTVAADTNNIGVAGM 93
QY 82 FPNLVKEQRV 92
Db 94 APDTKILAVRV 104

